

E value 9.0e-23
 Match length 133
 % identity 47
 NCBI Description cysteine proteinase - clove pink (fragment) >gi_595986
 (U17135) cysteine proteinase [Dianthus caryophyllus]

Seq. No. 232007
 Seq. ID LIB3197-044-Q1-M1-H4
 Method BLASTX
 NCBI GI g2252860
 BLAST score 113
 E value 9.0e-13
 Match length 109
 % identity 50
 NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No. 232008
 Seq. ID LIB3197-044-Q1-M1-H5
 Method BLASTX
 NCBI GI g3163946
 BLAST score 509
 E value 7.0e-52
 Match length 117
 % identity 85
 NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 232009
 Seq. ID LIB3197-044-Q1-M1-H6
 Method BLASTX
 NCBI GI g2832672
 BLAST score 194
 E value 4.0e-15
 Match length 64
 % identity 64
 NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No. 232010
 Seq. ID LIB3197-044-Q1-M1-H9
 Method BLASTX
 NCBI GI g4490332
 BLAST score 160
 E value 7.0e-11
 Match length 65
 % identity 55
 NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 232011
 Seq. ID LIB3197-045-Q1-M1-A10
 Method BLASTX
 NCBI GI g3182981
 BLAST score 550
 E value 1.0e-56
 Match length 130
 % identity 80
 NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_
 (D86494) diminuto [Pisum sativum]


```
Seq. No.      232017
Seq. ID       LIB3197-045-Q1-M1-B1
Method        BLASTX
NCBI GI       g4512667
BLAST score   383
E value       4.0e-37
Match length  109
% identity    69
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
```

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Seq. No.      232018
Seq. ID      LIB3197-045-Q1-M1-B10
Method       BLASTX
NCBI GI      g4508079
BLAST score   348
E value      7.0e-33
Match length  110
% identity    62
NCBI Description (AC005882) 66284 [Arabidopsis thaliana]
```

```
Seq. No.      232019
Seq. ID      LIB3197-045-Q1-M1-B11
Method       BLASTX
NCBI GI      g266944
BLAST score   597
E value      3.0e-62
Match length  117
% identity    95
NCBI Description 60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
>gi_71078_pir_R5TOL8 ribosomal protein L8, cytosolic -
tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein
L2 [Lycopersicon esculentum]
```

```
Seq. No.      232020
Seq. ID      LIB3197-045-Q1-M1-B12
Method       BLASTX
NCBI GI      g2791834
BLAST score   756
E value      1.0e-80
Match length  143
% identity    99
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
```

Seq. No.	232021
Seq. ID	LIB3197-045-Q1-M1-B2
Method	BLASTX
NCBI GI	g2829870
BLAST score	453
E value	3.0e-45
Match length	135
% identity	65
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

```
Seq. No.      232022
Seq. ID      LIB3197-045-Q1-M1-B3
Method      BLASTX
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Seq. No.      232031
Seq. ID       LIB3197-045-Q1-M1-C9
Method        BLASTX
NCBI GI       g464707
BLAST score   373
E value       6.0e-36
Match length  81
% identity    91
NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
protein S18.A - Arabidopsis thaliana
>gi_405613_emb_CAA80684_(Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343_emb_CAA82273_(Z28701)
S18 ribosomal protein [Arabidopsis thaliana]
>gi_434345_emb_CAA82274_(Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_(Z28962)
S18 ribosomal protein [Arabidopsis thaliana]
>gi_2505871_emb_CAA72909_(Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_(AL049482) S18.A ribosomal
protein [Arabidopsis thaliana]

```

```
Seq. No.      232032
Seq. ID       LIB3197-045-Q1-M1-D3
Method        BLASTX
NCBI GI       g2351374
BLAST score    438
E value       2.0e-43
Match length   97
% identity     86
NCBI Description (U54560) putative 26S proteasome subunit athMOV34
               [Arabidopsis thaliana]
```

```
Seq. No.      232033
Seq. ID       LIB3197-045-Q1-M1-D5
Method        BLASTX
NCBI GI       g4426565
BLAST score    158
E value       1.0e-10
Match length   144
% identity     26
NCBI Description (AF031483) unknown [Rattus norvegicus]
```

```
Seq. No.      232034
Seq. ID      LIB3197-045-Q1-M1-D6
Method       BLASTX
NCBI GI      g2088653
BLAST score   348
E value      7.0e-33
Match length  108
% identity   63
NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis thaliana]
```


Seq. No.	232035
Seq. ID	LIB3197-045-Q1-M1-D8
Method	BLASTX
NCBI GI	g2738248
BLAST score	410
E value	2.0e-40
Match length	99
% identity	79
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]
Seq. No.	232036
Seq. ID	LIB3197-045-Q1-M1-D9
Method	BLASTX
NCBI GI	g1931655
BLAST score	538
E value	3.0e-55
Match length	141
% identity	74
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]
Seq. No.	232037
Seq. ID	LIB3197-045-Q1-M1-E1
Method	BLASTX
NCBI GI	g465820
BLAST score	438
E value	2.0e-43
Match length	105
% identity	69
NCBI Description	HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III >gi_280536_pir_S28301 hypothetical protein C40H1.6 - Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154) C40H1.6 [Caenorhabditis elegans]
Seq. No.	232038
Seq. ID	LIB3197-045-Q1-M1-E10
Method	BLASTX
NCBI GI	g1174470
BLAST score	141
E value	4.0e-17
Match length	97
% identity	56
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf_2208301A integral membrane protein [Mus musculus]
Seq. No.	232039
Seq. ID	LIB3197-045-Q1-M1-E11
Method	BLASTX
NCBI GI	g4098129
BLAST score	394
E value	3.0e-38
Match length	95
% identity	83
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]

[Actinidia deliciosa]

Seq. No. 232045
Seq. ID LIB3197-045-Q1-M1-E9
Method BLASTX
NCBI GI g2499612
BLAST score 432
E value 5.0e-51
Match length 138
% identity 76
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (PMEK1)
>gi_1076650_pir_S52989 mitogen-activated,
extracellular-regulated protein kinase 1 (EC 2.7.1.-) -
garden petunia >gi_603871_emb_CAA58466_ (X83440) MAP/ERK
kinase_1 [Petunia x hybrida]

Seq. No. 232046
Seq. ID LIB3197-045-Q1-M1-F1
Method BLASTX
NCBI GI g2286153
BLAST score 402
E value 2.0e-39
Match length 83
% identity 96
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 232047
Seq. ID LIB3197-045-Q1-M1-F10
Method BLASTX
NCBI GI g4138137
BLAST score 566
E value 2.0e-58
Match length 134
% identity 71
NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No. 232048
Seq. ID LIB3197-045-Q1-M1-F11
Method BLASTX
NCBI GI g126896
BLAST score 611
E value 9.0e-64
Match length 132
% identity 90
NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
>gi_319831_pir_DEPUMW malate dehydrogenase (EC 1.1.1.37)
precursor, mitochondrial - watermelon
>gi_18297_emb_CAA35239_ (X17362) precursor protein (AA¹-27
to 320) [Citrullus lanatus]

Seq. No. 232049
Seq. ID LIB3197-045-Q1-M1-F12
Method BLASTX
NCBI GI g2499607
BLAST score 719
E value 2.0e-76
Match length 139

% identity	94
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3) (ATMPK3) >gi_629544_pir_S40469 mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457398_dbj_BAA04866_ (D21839) MAP kinase [Arabidopsis thaliana]
Seq. No.	232050
Seq. ID	LIB3197-045-Q1-M1-F2
Method	BLASTX
NCBI GI	g3650378
BLAST score	156
E value	2.0e-10
Match length	56
% identity	52
NCBI Description	(AL031740) putative rRNA biogenesis protein; rrp5 homolog; multiple S1 rna binding domain protein [Schizosaccharomyces pombe]
Seq. No.	232051
Seq. ID	LIB3197-045-Q1-M1-F4
Method	BLASTX
NCBI GI	g3493172
BLAST score	623
E value	4.0e-65
Match length	133
% identity	92
NCBI Description	(U89609) fiber annexin [Gossypium hirsutum]
Seq. No.	232052
Seq. ID	LIB3197-045-Q1-M1-F5
Method	BLASTX
NCBI GI	g2245378
BLAST score	679
E value	1.0e-71
Match length	139
% identity	88
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]
Seq. No.	232053
Seq. ID	LIB3197-045-Q1-M1-F6
Method	BLASTX
NCBI GI	g125887
BLAST score	223
E value	3.0e-18
Match length	115
% identity	44
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir_S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]
Seq. No.	232054
Seq. ID	LIB3197-045-Q1-M1-F7
Method	BLASTX
NCBI GI	g3334115
BLAST score	457

E value 9.0e-46
 Match length 97
 % identity 93
 NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

Seq. No. 232055
 Seq. ID LIB3197-045-Q1-M1-F8
 Method BLASTX
 NCBI GI g3080420
 BLAST score 497
 E value 2.0e-50
 Match length 121
 % identity 75
 NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 232056
 Seq. ID LIB3197-045-Q1-M1-F9
 Method BLASTX
 NCBI GI g870726
 BLAST score 427
 E value 4.0e-42
 Match length 116
 % identity 76
 NCBI Description (L38260) biotin carboxylase subunit [Nicotiana tabacum] >gi_1582354_prf_2118337A Ac-CoA carboxylase:SUBUNIT=biotin carboxylase [Nicotiana tabacum]

Seq. No. 232057
 Seq. ID LIB3197-045-Q1-M1-G3
 Method BLASTX
 NCBI GI g1946355
 BLAST score 358
 E value 4.0e-34
 Match length 124
 % identity 56
 NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 232058
 Seq. ID LIB3197-045-Q1-M1-G4
 Method BLASTX
 NCBI GI g4544409
 BLAST score 404
 E value 2.0e-39
 Match length 123
 % identity 63
 NCBI Description (AC006955) putative transcription factor [Arabidopsis thaliana]

Seq. No. 232059
 Seq. ID LIB3197-045-Q1-M1-G6
 Method BLASTX

NCBI GI g2129578
 BLAST score 224
 E value 1.0e-33
 Match length 139
 % identity 62
 NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf_2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No. 232060
 Seq. ID LIB3197-045-Q1-M1-G8
 Method BLASTX
 NCBI GI g3242705
 BLAST score 354
 E value 1.0e-33
 Match length 82
 % identity 77
 NCBI Description (AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No. 232061
 Seq. ID LIB3197-045-Q1-M1-H11
 Method BLASTX
 NCBI GI g1220196
 BLAST score 586
 E value 8.0e-61
 Match length 131
 % identity 85
 NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 232062
 Seq. ID LIB3197-045-Q1-M1-H4
 Method BLASTX
 NCBI GI g4098128
 BLAST score 589
 E value 4.0e-61
 Match length 130
 % identity 88
 NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 232063
 Seq. ID LIB3197-045-Q1-M1-H7
 Method BLASTX
 NCBI GI g1707017
 BLAST score 685
 E value 2.0e-72
 Match length 143
 % identity 92
 NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 232064
 Seq. ID LIB3197-045-Q1-M1-H9
 Method BLASTX
 NCBI GI g3925703
 BLAST score 578

% identity	56
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.	232070
Seq. ID	LIB3197-046-Q1-M1-B1
Method	BLASTX
NCBI GI	g3128234
BLAST score	338
E value	1.0e-31
Match length	110
% identity	66
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]
Seq. No.	232071
Seq. ID	LIB3197-046-Q1-M1-B11
Method	BLASTX
NCBI GI	g4056494
BLAST score	368
E value	3.0e-35
Match length	88
% identity	76
NCBI Description	(AC005896) putative protein translocase [Arabidopsis thaliana]
Seq. No.	232072
Seq. ID	LIB3197-046-Q1-M1-B12
Method	BLASTX
NCBI GI	g4193388
BLAST score	489
E value	3.0e-56
Match length	137
% identity	83
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]
Seq. No.	232073
Seq. ID	LIB3197-046-Q1-M1-B4
Method	BLASTX
NCBI GI	g2497753
BLAST score	185
E value	4.0e-14
Match length	48
% identity	62
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]
Seq. No.	232074
Seq. ID	LIB3197-046-Q1-M1-B6
Method	BLASTX
NCBI GI	g728880
BLAST score	443
E value	4.0e-46
Match length	139
% identity	69
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase

Seq. No. 232085
 Seq. ID LIB3197-046-Q1-M1-D7
 Method BLASTX
 NCBI GI g4406780
 BLAST score 237
 E value 6.0e-20
 Match length 53
 % identity 83
 NCBI Description (AC006532) putative multispinning membrane protein
 [Arabidopsis thaliana]

Seq. No. 232086
 Seq. ID LIB3197-046-Q1-M1-D9
 Method BLASTX
 NCBI GI g4056478
 BLAST score 291
 E value 3.0e-26
 Match length 96
 % identity 65
 NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 232087
 Seq. ID LIB3197-046-Q1-M1-E10
 Method BLASTX
 NCBI GI g2673868
 BLAST score 383
 E value 5.0e-37
 Match length 104
 % identity 77
 NCBI Description (Y14856) fimbriata-associated protein [Antirrhinum majus]

Seq. No. 232088
 Seq. ID LIB3197-046-Q1-M1-E5
 Method BLASTX
 NCBI GI g2341034
 BLAST score 535
 E value 7.0e-55
 Match length 110
 % identity 96
 NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No. 232089
 Seq. ID LIB3197-046-Q1-M1-E6
 Method BLASTX
 NCBI GI g3608137
 BLAST score 329
 E value 1.0e-30
 Match length 119
 % identity 54
 NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 232090
 Seq. ID LIB3197-046-Q1-M1-F10
 Method BLASTX
 NCBI GI g4580389
 BLAST score 604
 E value 6.0e-63

Match length	137
% identity	80
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.	232091
Seq. ID	LIB3197-046-Q1-M1-F12
Method	BLASTX
NCBI GI	g1362152
BLAST score	238
E value	5.0e-20
Match length	85
% identity	49
NCBI Description	ribosomal protein S6 kinase homolog (clone Aspk11) - oat >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]
Seq. No.	232092
Seq. ID	LIB3197-046-Q1-M1-F6
Method	BLASTX
NCBI GI	g2500354
BLAST score	625
E value	2.0e-65
Match length	119
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]
Seq. No.	232093
Seq. ID	LIB3197-046-Q1-M1-F7
Method	BLASTX
NCBI GI	g125051
BLAST score	340
E value	3.0e-32
Match length	83
% identity	81
NCBI Description	ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD) >gi_88038_pir_A37033 isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human >gi_306897 (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens] >gi_4504799_ref_NP_002216.1_pIVD_ isovaleryl Coenzyme A dehydrogenase
Seq. No.	232094
Seq. ID	LIB3197-046-Q1-M1-F8
Method	BLASTX
NCBI GI	g3668089
BLAST score	298
E value	3.0e-27
Match length	104
% identity	51
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	232095
Seq. ID	LIB3197-046-Q1-M1-F9
Method	BLASTX
NCBI GI	g475598
BLAST score	301

Seq. No. 232111
 Seq. ID LIB3197-046-Q1-M1-H8
 Method BLASTX
 NCBI GI g3043428
 BLAST score 326
 E value 2.0e-30
 Match length 96
 % identity 74
 NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 232112
 Seq. ID LIB3197-047-Q1-M1-A1
 Method BLASTX
 NCBI GI g3420751
 BLAST score 343
 E value 2.0e-32
 Match length 121
 % identity 52
 NCBI Description (AF079448) cytochrome c oxidase assembly protein [Dictyostelium discoideum]

Seq. No. 232113
 Seq. ID LIB3197-047-Q1-M1-A10
 Method BLASTX
 NCBI GI g1168972
 BLAST score 369
 E value 2.0e-35
 Match length 115
 % identity 42
 NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA PRECURSOR >gi_480969_pir_S37557 clpA protein - rape (fragment) >gi_406311_emb_CAA53077_ (X75328) clpA [Brassica napus]

Seq. No. 232114
 Seq. ID LIB3197-047-Q1-M1-A11
 Method BLASTX
 NCBI GI g2160151
 BLAST score 362
 E value 1.0e-34
 Match length 122
 % identity 61
 NCBI Description (AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No. 232115
 Seq. ID LIB3197-047-Q1-M1-A2
 Method BLASTX
 NCBI GI g1107526
 BLAST score 142
 E value 1.0e-08
 Match length 59
 % identity 42
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 232116
 Seq. ID LIB3197-047-Q1-M1-A4


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BLAST score      514
E value         3.0e-52
Match length    119
% identity      82
NCBI Description (AC005966) Strong similarity to gi_3337350.F13P17.3~
putative permease from Arabidopsis thaliana BAC
qb AC004481. [Arabidopsis thaliana]
```

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Seq. No.          232127
Seq. ID          LIB3197-047-Q1-M1-C2
Method           BLASTX
NCBI GI          g3142294
BLAST score      378
E value          2.0e-36
Match length     83
% identity       87
NCBI Description  (AC002411) Strong similarity to initiation factor eIF-2,
                  gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and
                  gb_N37529 come from this gene. [Arabidopsis thaliana]
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Seq. No.          232128
Seq. ID           LIB3197-047-Q1-M1-C3
Method            BLASTX
NCBI GI           g627469
BLAST score       244
E value           1.0e-20
Match length      140
% identity        8
NCBI Description   hypothetical protein 2 - human (fragment)
```

```
Seq. No.      232129
Seq. ID      LIB3197-047-Q1-M1-C5
Method       BLASTX
NCBI GI      g832876
BLAST score   639
E value      6.0e-67
Match length  140
% identity    89
NCBI Description (L41345) ascorbate free radical reductase [Solanum
lycopersicum] >gi_1097368_prf_2113407A ascorbate free
radical reductase [Lycopersicon esculentum]
```

```
Seq. No.      232130
Seq. ID      LIB3197-047-Q1-M1-C6
Method       BLASTX
NCBI GI      g2213590
BLAST score   215
E value      2.0e-21
Match length 102
% identity   51
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]
```

```
Seq. No.      232131
Seq. ID       LIB3197-047-Q1-M1-C7
Method        BLASTX
NCBI GI       g267069
BLAST score    648
```


E value 5.0e-68
 Match length 120
 % identity 98
 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594
 tubulin alpha chain - Arabidopsis thaliana >gi_166914
 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 232132
 Seq. ID LIB3197-047-Q1-M1-C8
 Method BLASTX
 NCBI GI g1350944
 BLAST score 386
 E value 2.0e-37
 Match length 80
 % identity 95
 NCBI Description 40S RIBOSOMAL PROTEIN S17

Seq. No. 232133
 Seq. ID LIB3197-047-Q1-M1-C9
 Method BLASTX
 NCBI GI g485126
 BLAST score 175
 E value 1.0e-12
 Match length 73
 % identity 51
 NCBI Description (U00052) similar to RNA binding proteins [Caenorhabditis elegans]

Seq. No. 232134
 Seq. ID LIB3197-047-Q1-M1-D10
 Method BLASTX
 NCBI GI g586038
 BLAST score 718
 E value 3.0e-76
 Match length 152
 % identity 94
 NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN CHLOROPLAST
 PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC)
 >gi_480296_pir_S36637 signal recognition particle 54CP
 protein precursor - Arabidopsis thaliana
 >gi_396701_emb_CAA79981_ (Z21970) 54CP [Arabidopsis thaliana]

Seq. No. 232135
 Seq. ID LIB3197-047-Q1-M1-D11
 Method BLASTX
 NCBI GI g120669
 BLAST score 523
 E value 2.0e-53
 Match length 122
 % identity 82
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
 dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
 >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
 3-phosphate dehydrogenase [Magnolia liliiflora]


```
Seq. No.      232136
Seq. ID      LIB3197-047-Q1-M1-D12
Method       BLASTX
NCBI GI      g119351
BLAST score   203
E value      8.0e-16
Match length  52
% identity    77
NCBI Description  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_84950_pir_S07586
                phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly
                (Drosophila melanogaster) >gi_7946_emb_CAA34895_ (X17034)
                enolase (AA 1-433) [Drosophila melanogaster]
```

```
Seq. No.      232137
Seq. ID      LIB3197-047-Q1-M1-D3
Method       BLASTX
NCBI GI      g135535
BLAST score   300
E value      2.0e-27
Match length  67
% identity   88
NCBI Description  T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
                  (CCT-ALPHA) >gi_322602_pir_JN0448 t-complex polypeptide
                  Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955
                  (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                  thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                  alpha/TCP-1 [Arabidopsis thaliana]
```

```
Seq. No.      232138
Seq. ID       LIB3197-047-Q1-M1-D5
Method        BLASTX
NCBI GI       g2102696
BLAST score   259
E value       2.0e-22
Match length  128
% identity    38
NCBI Description (U72761) karyopherin beta 3 [Homo sapiens]
               >gi_4504909_ref_NP_002262.1_pKPNB3_ karyopherin (importin)
               beta
```

```

Seq. No.      232139
Seq. ID       LIB3197-047-Q1-M1-D8
Method        BLASTX
NCBI GI       g1169534
BLAST score   645
E value       9.0e-68
Match length  134
% identity    93
NCBI Description  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir_S39203
                phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus
                communis]

```

Seq. No. 232140


```
BLAST score      303
E value         1.0e-27
Match length    118
% identity      57
NCBI Description (AB016063) mitochondrial phosphate transporter [Glycine
max]
```

```
Seq. No.      232146
Seq. ID      LIB3197-047-Q1-M1-F8
Method       BLASTX
NCBI GI      g586076
BLAST score   615
E value      2.0e-64
Match length 115
% identity   97
NCBI Description TUBULIN BETA-1 CHAIN >gi_486734_pir_S35142 tubulin beta
chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
tubulin 1 [Lupinus albus]
```

```
Seq. No.      232147
Seq. ID      LIB3197-047-Q1-M1-F9
Method       BLASTX
NCBI GI      g2431769
BLAST score   233
E value      1.0e-23
Match length  78
% identity    78
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
```

```
Seq. No.          232148
Seq. ID           LIB3197-047-Q1-M1-G1
Method            BLASTX
NCBI GI           g2811278
BLAST score       651
E value           2.0e-68
Match length      133
% identity         88
NCBI Description   (AF043284) expansin [Gossypium hirsutum]
```

```
Seq. No.      232149
Seq. ID       LIB3197-047-Q1-M1-G10
Method        BLASTX
NCBI GI       g3176387
BLAST score   473
E value       1.0e-47
Match length   99
% identity    85
NCBI Description (AB009849) neuropsin [Homo sapiens]
```

```
Seq. No.      232150
Seq. ID      LIB3197-047-Q1-M1-G11
Method       BLASTX
NCBI GI      g399082
BLAST score   148
E value      2.0e-09
Match length  112
% identity    37
```


0664016 10100

Match length 102
 % identity 67
 NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir_JN0718
 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
 precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
 (D13042) thiol protease [Arabidopsis thaliana]
 >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
 cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 232167
 Seq. ID LIB3197-048-Q1-M1-B10
 Method BLASTX
 NCBI GI g4539324
 BLAST score 205
 E value 4.0e-19
 Match length 134
 % identity 46
 NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 232168
 Seq. ID LIB3197-048-Q1-M1-B11
 Method BLASTX
 NCBI GI g1155261
 BLAST score 347
 E value 8.0e-33
 Match length 95
 % identity 74
 NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis
 thaliana]

Seq. No. 232169
 Seq. ID LIB3197-048-Q1-M1-B4
 Method BLASTX
 NCBI GI g2961300
 BLAST score 517
 E value 1.0e-52
 Match length 107
 % identity 93
 NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]

Seq. No. 232170
 Seq. ID LIB3197-048-Q1-M1-B5
 Method BLASTX
 NCBI GI g3914097
 BLAST score 191
 E value 1.0e-14
 Match length 68
 % identity 60
 NCBI Description MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL
 MONOPHOSPHATASE) >gi_2708322 (AF037220) inositol
 monophosphatase [Mesembryanthemum crystallinum]

Seq. No. 232171
 Seq. ID LIB3197-048-Q1-M1-B6
 Method BLASTX
 NCBI GI g3522929
 BLAST score 708

09010100

```
Seq. No.      232177
Seq. ID      LIB3197-048-Q1-M1-D6
Method       BLASTX
NCBI GI      g2894612
BLAST score   571
E value      4.0e-59
Match length  128
% identity    77
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      232179
Seq. ID      LIB3197-048-Q1-M1-H2
Method       BLASTX
NCBI GI      g1296805
BLAST score   208
E value      1.0e-16
Match length  55
% identity    64
NCBI Description (X90929) C-terminal peptidase of the D1 protein [Hordeum
vulgare]
```

Seq. No. 232181

Seq. ID LIB3197-048-Q1-M1-H7
 Method BLASTX
 NCBI GI g3282505
 BLAST score 202
 E value 8.0e-16
 Match length 134
 % identity 45
 NCBI Description (AF020786) polyphenol oxidase precursor [Prunus armeniaca]

Seq. No. 232182
 Seq. ID LIB3197-048-Q1-M1-H9
 Method BLASTX
 NCBI GI g2129887
 BLAST score 269
 E value 1.0e-23
 Match length 132
 % identity 45
 NCBI Description major inner envelope protein precursor, 96K, chloroplast - garden pea

Seq. No. 232183
 Seq. ID LIB3197-049-Q1-M1-A1
 Method BLASTX
 NCBI GI g3513738
 BLAST score 327
 E value 2.0e-30
 Match length 91
 % identity 69
 NCBI Description (AF080118). similar to the GDSL family of lipolytic enzymes [Arabidopsis thaliana]

Seq. No. 232184
 Seq. ID LIB3197-049-Q1-M1-A10
 Method BLASTX
 NCBI GI g2618689
 BLAST score 364
 E value 3.0e-35
 Match length 78
 % identity 90
 NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 232185
 Seq. ID LIB3197-049-Q1-M1-A12
 Method BLASTX
 NCBI GI g4239845
 BLAST score 478
 E value 2.0e-48
 Match length 101
 % identity 92
 NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 232186
 Seq. ID LIB3197-049-Q1-M1-A5
 Method BLASTX
 NCBI GI g4455323
 BLAST score 280
 E value 3.0e-25

Match length 72
 % identity 72
 NCBI Description (AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 232187
 Seq. ID LIB3197-049-Q1-M1-A7
 Method BLASTX
 NCBI GI g1213629
 BLAST score 342
 E value 4.0e-32
 Match length 93
 % identity 70
 NCBI Description (X95991) pectinesterase [Prunus persica]

Seq. No. 232188
 Seq. ID LIB3197-049-Q1-M1-A9
 Method BLASTX
 NCBI GI g4567235
 BLAST score 365
 E value 8.0e-35
 Match length 114
 % identity 61
 NCBI Description (AC007119) putative phosphatidylinositol/phosphatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No. 232189
 Seq. ID LIB3197-049-Q1-M1-B10
 Method BLASTX
 NCBI GI g3668089
 BLAST score 212
 E value 6.0e-17
 Match length 78
 % identity 47
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 232190
 Seq. ID LIB3197-049-Q1-M1-B2
 Method BLASTX
 NCBI GI g3738320
 BLAST score 257
 E value 4.0e-22
 Match length 123
 % identity 43
 NCBI Description (AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No. 232191
 Seq. ID LIB3197-049-Q1-M1-B3
 Method BLASTX
 NCBI GI g1477468
 BLAST score 114
 E value 7.0e-12
 Match length 85
 % identity 46
 NCBI Description (U35244) vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]

E value 1.0e-29
 Match length 84
 % identity 76
 NCBI Description (L38260) biotin carboxylase subunit [Nicotiana tabacum]
 >gi_1582354_prf_2118337A Ac-CoA carboxylase:SUBUNIT=biotin
 carboxylase [Nicotiana tabacum]

Seq. No. 232203
 Seq. ID LIB3197-049-Q1-M1-D2
 Method BLASTX
 NCBI GI g3097321
 BLAST score 196
 E value 3.0e-15
 Match length 88
 % identity 44
 NCBI Description (AB013289) Bd 30K [Glycine max]

Seq. No. 232204
 Seq. ID LIB3197-049-Q1-M1-D4
 Method BLASTX
 NCBI GI g3132696
 BLAST score 436
 E value 2.0e-43
 Match length 98
 % identity 85
 NCBI Description (AF061962) SAR DNA-binding protein-1 [Pisum sativum]

Seq. No. 232205
 Seq. ID LIB3197-049-Q1-M1-D6
 Method BLASTX
 NCBI GI g133940
 BLAST score 557
 E value 2.0e-57
 Match length 124
 % identity 92
 NCBI Description 40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir_R3XL3A
 ribosomal protein S3a - African clawed frog
 >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a
 [Xenopus laevis]

Seq. No. 232206
 Seq. ID LIB3197-049-Q1-M1-D9
 Method BLASTX
 NCBI GI g4204300
 BLAST score 188
 E value 3.0e-14
 Match length 72
 % identity 54
 NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 232207
 Seq. ID LIB3197-049-Q1-M1-E1
 Method BLASTX
 NCBI GI g4220512
 BLAST score 188
 E value 4.0e-14
 Match length 57

NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
arietinum]

Seq. No. 232213
Seq. ID LIB3197-049-Q1-M1-F1
Method BLASTX
NCBI GI g3702339
BLAST score 149
E value 9.0e-10
Match length 55
% identity 62
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 232214
Seq. ID LIB3197-049-Q1-M1-F12
Method BLASTX
NCBI GI g2842490
BLAST score 431
E value 1.0e-42
Match length 120
% identity 70
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 232215
Seq. ID LIB3197-049-Q1-M1-F4
Method BLASTX
NCBI GI g4510406
BLAST score 543
E value 9.0e-56
Match length 130
% identity 76
NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No. 232216
Seq. ID LIB3197-049-Q1-M1-F5
Method BLASTX
NCBI GI g2129499
BLAST score 289
E value 6.0e-26
Match length 52
% identity 100
NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton
>gi_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No. 232217
Seq. ID LIB3197-049-Q1-M1-G5
Method BLASTX
NCBI GI g2558654
BLAST score 365
E value 7.0e-35
Match length 114
% identity 54
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 232218
Seq. ID LIB3197-049-Q1-M1-G6
Method BLASTX

E value 3.0e-15
 Match length 139
 % identity 32
 NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]
 >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
 protein [Arabidopsis thaliana]

Seq. No. 232254
 Seq. ID LIB3197-050-Q1-M1-F1
 Method BLASTX
 NCBI GI g2738949
 BLAST score 602
 E value 1.0e-62
 Match length 123
 % identity 89
 NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x
 ananassa]

Seq. No. 232255
 Seq. ID LIB3197-050-Q1-M1-F10
 Method BLASTX
 NCBI GI g1771162
 BLAST score 441
 E value 7.0e-44
 Match length 123
 % identity 71
 NCBI Description (X98930) SBT2 [Lycopersicon esculentum]
 >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like
 protease [Lycopersicon esculentum]

Seq. No. 232256
 Seq. ID LIB3197-050-Q1-M1-F12
 Method BLASTX
 NCBI GI g3193288
 BLAST score 531
 E value 2.0e-54
 Match length 135
 % identity 70
 NCBI Description (AF069298) similar to bacterial and fungi pectinesterases
 [Arabidopsis thaliana]

Seq. No. 232257
 Seq. ID LIB3197-050-Q1-M1-F2
 Method BLASTX
 NCBI GI g135406
 BLAST score 597
 E value 4.0e-62
 Match length 116
 % identity 96
 NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir_A32712 tubulin
 alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
 alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
 alpha-5 tubulin [Arabidopsis thaliana]

Seq. No. 232258
 Seq. ID LIB3197-050-Q1-M1-F3
 Method BLASTX

BLAST score 481
 E value 2.0e-48
 Match length 112
 % identity 85
 NCBI Description (AJ225172) magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum]

Seq. No. 232283
 Seq. ID LIB3197-051-Q1-M1-D2
 Method BLASTX
 NCBI GI g2244749
 BLAST score 433
 E value 5.0e-43
 Match length 88
 % identity 93
 NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 232284
 Seq. ID LIB3197-051-Q1-M1-D4
 Method BLASTX
 NCBI GI g3687237
 BLAST score 341
 E value 3.0e-32
 Match length 111
 % identity 59
 NCBI Description (AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No. 232285
 Seq. ID LIB3197-051-Q1-M1-D5
 Method BLASTX
 NCBI GI g1362086
 BLAST score 372
 E value 2.0e-38
 Match length 124
 % identity 73
 NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir_S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No. 232286
 Seq. ID LIB3197-051-Q1-M1-D6
 Method BLASTX
 NCBI GI g3334115
 BLAST score 194
 E value 2.0e-27
 Match length 83
 % identity 78
 NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]


```
Seq. No.      232292
Seq. ID      LIB3197-051-Q1-M1-E8
Method       BLASTX
NCBI GI      g2497753
BLAST score   376
E value      3.0e-36
Match length  123
% identity    55
NCBI Description  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                [Prunus dulcis]
```

```
Seq. No.      232293
Seq. ID      LIB3197-051-Q1-M1-F1
Method       BLASTX
NCBI GI      g3913366
BLAST score   294
E value      9.0e-27
Match length  94
% identity    61
NCBI Description  PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR
                >qi_1597723 (U67422) CRINKLY4 precursor [Zea mays]
```

```
Seq. No.      232294
Seq. ID      LIB3197-051-Q1-M1-F10
Method       BLASTX
NCBI GI      g267069
BLAST score   688
E value      1.0e-72
Match length  130
% identity    98
NCBI Description  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) alpha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
```

```
Seq. No.      232295
Seq. ID      LFB3197-051-Q1-M1-F11
Method       BLASTX
NCBI GI      g485742
BLAST score   731
E value      9.0e-78
Match length  149
% identity    99
NCBI Description (L32791) pyrophosphatase [Beta vulgaris]
```

```
Seq. No.      232296
Seq. ID      LIB3197-051-Q1-M1-F12
Method       BLASTX
NCBI GI      g4580389
BLAST score   509
E value      8.0e-52
Match length  130
% identity    73
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
```


Match length	91
% identity	86
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]
Seq. No.	232313
Seq. ID	LIB3197-052-Q1-M1-A12
Method	BLASTX
NCBI GI	g1174592
BLAST score	724
E value	5.0e-77
Match length	137
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]
Seq. No.	232314
Seq. ID	LIB3197-052-Q1-M1-A2
Method	BLASTX
NCBI GI	g2662341
BLAST score	693
E value	2.0e-73
Match length	133
% identity	98
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]
Seq. No.	232315
Seq. ID	LIB3197-052-Q1-M1-A4
Method	BLASTX
NCBI GI	g1843527
BLAST score	491
E value	1.0e-49
Match length	129
% identity	44
NCBI Description	(U73747) annexin [Gossypium hirsutum]
Seq. No.	232316
Seq. ID	LIB3197-052-Q1-M1-A5
Method	BLASTX
NCBI GI	g464849
BLAST score	628
E value	1.0e-65
Match length	142
% identity	88
NCBI Description	TUBULIN ALPHA CHAIN >gi_486847_pir_S36232 tubulin alpha chain - almond >gi_20413_emb_CAA47635_ (X67162) alpha-tubulin [Prunus dulcis]
Seq. No.	232317
Seq. ID	LIB3197-052-Q1-M1-A6
Method	BLASTX
NCBI GI	g3757514
BLAST score	352

E value	2.0e-33
Match length	71
% identity	93
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]
Seq. No.	232318
Seq. ID	LIB3197-052-Q1-M1-A7
Method	BLASTX
NCBI GI	g1155261
BLAST score	379
E value	1.0e-36
Match length	85
% identity	88
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]
Seq. No.	232319
Seq. ID	LIB3197-052-Q1-M1-A8
Method	BLASTX
NCBI GI	g1703129
BLAST score	544
E value	6.0e-56
Match length	103
% identity	98
NCBI Description	ACTIN 11 >gi_2129522_pir_S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]
Seq. No.	232320
Seq. ID	LIB3197-052-Q1-M1-B1
Method	BLASTX
NCBI GI	g3874433
BLAST score	220
E value	7.0e-18
Match length	106
% identity	42
NCBI Description	(Z81038) predicted using Genefinder; Similarity to Yeast ABD1 protein (SW:P32783); cDNA EST EMBL:T01105 comes from this gene [Caenorhabditis elegans]
Seq. No.	232321
Seq. ID	LIB3197-052-Q1-M1-B12
Method	BLASTX
NCBI GI	g2104681
BLAST score	359
E value	3.0e-34
Match length	132
% identity	60
NCBI Description	(X97907) transcription factor [Vicia faba]
Seq. No.	232322
Seq. ID	LIB3197-052-Q1-M1-B3
Method	BLASTX
NCBI GI	g2832643
BLAST score	167
E value	1.0e-11

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Seq. No.	232334
Seq. ID	LIB3197-052-Q1-M1-D11
Method	BLASTX
NCBI GI	g2062167
BLAST score	489
E value	2.0e-49
Match length	105
% identity	86
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana].

```
Seq. No.      232336
Seq. ID      LIB3197-052-Q1-M1-D3
Method       BLASTX
NCBI GI      g1361155
BLAST score   150
E value      1.0e-09
Match length  66
% identity    53
NCBI Description  hypothetical protein o215b - Escherichia coli >gi_537235
                  (U14003) Kenn Rudd identifies as gpmB [Escherichia coli]
                  >gi_1790856 (AE000509) phosphoglyceromutase 2 [Escherichia
                  coli]
```

3.3466

00684016-101000

[Catharanthus roseus]

Seq. No. 232347
 Seq. ID LIB3197-052-Q1-M1-F11
 Method BLASTX
 NCBI GI g3128175
 BLAST score 142
 E value 7.0e-09
 Match length 88
 % identity 36
 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 232348
 Seq. ID LIB3197-052-Q1-M1-F2
 Method BLASTX
 NCBI GI g2130073
 BLAST score 524
 E value 2.0e-53
 Match length 122
 % identity 85
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 232349
 Seq. ID LIB3197-052-Q1-M1-F3
 Method BLASTX
 NCBI GI g2130073
 BLAST score 330
 E value 7.0e-31
 Match length 85
 % identity 80
 NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 232350
 Seq. ID LIB3197-052-Q1-M1-F5
 Method BLASTX
 NCBI GI g4455192
 BLAST score 380
 E value 1.0e-36
 Match length 140
 % identity 38
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 232351
 Seq. ID LIB3197-052-Q1-M1-F6
 Method BLASTX
 NCBI GI g425194
 BLAST score 573
 E value 3.0e-59
 Match length 121
 % identity 90
 NCBI Description (L26243) heat shock protein [Spinacia oleracea] >gi_2660772

(AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 232352
Seq. ID LIB3197-052-Q1-M1-F7
Method BLASTX
NCBI GI g1890281
BLAST score 336
E value 2.0e-31
Match length 103
% identity 22
NCBI Description (U89984) transformation-sensitive protein homolog [Acanthamoeba castellanii]

Seq. No. 232353
Seq. ID LIB3197-052-Q1-M1-F8
Method BLASTX
NCBI GI g1771780
BLAST score 492
E value 7.0e-50
Match length 125
% identity 82
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 232354
Seq. ID LIB3197-052-Q1-M1-F9
Method BLASTX
NCBI GI g2827621
BLAST score 411
E value 3.0e-40
Match length 98
% identity 79
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 232355
Seq. ID LIB3197-052-Q1-M1-G10
Method BLASTX
NCBI GI g4006893
BLAST score 288
E value 5.0e-26
Match length 60
% identity 92
NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 232356
Seq. ID LIB3197-052-Q1-M1-G12
Method BLASTX
NCBI GI g559713
BLAST score 216
E value 2.0e-17
Match length 108
% identity 40
NCBI Description (D38552) The ha1539 protein is related to cyclophilin. [Homo sapiens]

Seq. No. 232357
Seq. ID LIB3197-052-Q1-M1-G4

09631015 101000

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Seq. No.      232364
Seq. ID      LIB3197-053-Q1-M1-A3
Method       BLASTX
NCBI GI      g1749546
BLAST score   223
E value      4.0e-18
Match length  98
% identity   52
NCBI Description (D89169) similar to Saccharomyces cerevisiae SCD6 protein,
               SWISS-PROT Accession Number P45978 [Schizosaccharomyces
               pombe]
```

```
Seq. No.      232366
Seq. ID      LIB3197-053-Q1-M1-A6
Method       BLASTX
NCBI GI      g2792364
BLAST score   148
E value      2.0e-09
Match length  150
% identity    26
NCBI Description (AF040964) unknown protein IT1 [Homo sapiens]
```

33472

% identity	81
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	232368
Seq. ID	LIB3197-053-Q1-M1-A9
Method	BLASTX
NCBI GI	g2494905
BLAST score	220
E value	8.0e-18
Match length	126
% identity	41
NCBI Description	MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi_2132107_pir__S67174 hypothetical protein YOR272w - yeast (Saccharomyces cerevisiae) >gi_1279699_emb_CAA61778_ (X89633) hypothetical protein [Saccharomyces cerevisiae] >gi_1420610_emb_CAA99497_ (Z75180) ORF YOR272w [Saccharomyces cerevisiae] >gi_1928989 (U92821) microtubule-associated protein [Saccharomyces cerevisiae]
Seq. No.	232369
Seq. ID	LIB3197-053-Q1-M1-B2
Method	BLASTX
NCBI GI	g4204695
BLAST score	276
E value	1.0e-24
Match length	118
% identity	53
NCBI Description	(AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]
Seq. No.	232370
Seq. ID	LIB3197-053-Q1-M1-B3
Method	BLASTX
NCBI GI	g3355486
BLAST score	384
E value	4.0e-37
Match length	124
% identity	63
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.	232371
Seq. ID	LIB3197-053-Q1-M1-B6
Method	BLASTX
NCBI GI	g2983325
BLAST score	142
E value	1.0e-08
Match length	81
% identity	33
NCBI Description	(AE000705) hypothetical protein [Aquifex aeolicus]
Seq. No.	232372
Seq. ID	LIB3197-053-Q1-M1-C2
Method	BLASTX
NCBI GI	g1705678
BLAST score	291
E value	2.0e-26
Match length	92

% identity 50
 NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
 PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
 valosin-containing protein [Glycine max]

Seq. No. 232373
 Seq. ID LIB3197-053-Q1-M1-C4
 Method BLASTX
 NCBI GI g2244734
 BLAST score 258
 E value 1.0e-22
 Match length 57
 % identity 89
 NCBI Description (D88414) actin [Gossypium hirsutum]

Seq. No. 232374
 Seq. ID LIB3197-053-Q1-M1-C5
 Method BLASTX
 NCBI GI g3914468
 BLAST score 437
 E value 2.0e-43
 Match length 112
 % identity 79
 NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
 >gi_478411_pir_JQ2257 nuclear antigen 21D7 - carrot
 >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus
 carota]

Seq. No. 232375
 Seq. ID LIB3197-053-Q1-M1-C6
 Method BLASTX
 NCBI GI g2789660
 BLAST score 224
 E value 1.0e-18
 Match length 74
 % identity 64
 NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 232376
 Seq. ID LIB3197-053-Q1-M1-C7
 Method BLASTX
 NCBI GI g4220535
 BLAST score 152
 E value 6.0e-18
 Match length 121
 % identity 54
 NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis
 thaliana]

Seq. No. 232377
 Seq. ID LIB3197-053-Q1-M1-D11
 Method BLASTX
 NCBI GI g3834321
 BLAST score 439
 E value 1.0e-43
 Match length 134
 % identity 72


```
Seq. No.      232383
Seq. ID      LIB3197-053-Q1-M1-E7
Method       BLASTX
NCBI GI      g129916
BLAST score   714
E value      9.0e-76
Match length  152
% identity    93
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY
phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
(AA_1 - 401) [Triticum aestivum]
```

```
Seq. No.      232384
Seq. ID      LIB3197-053-Q1-M1-F11
Method       BLASTX
NCBI GI      g2281094
BLAST score   463
E value      2.0e-46
Match length  124
% identity    70
NCBI Description (AC002333) molybdenum cofactor biosynthesis protein E
isolog [Arabidopsis thaliana] >gi_4469121_emb_CAB38428_
(AJ133519) molybdopterin synthase large subunit
[Arabidopsis thaliana]
```

```
Seq. No.      232385
Seq. ID      LIB3197-053-Q1-M1-F12
Method       BLASTX
NCBI GI      g2583108
BLAST score   567
E value      2.0e-58
Match length  152
% identity    76
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
```

```
Seq. No.      232386
Seq. ID      LIB3197-053-Q1-M1-F2
Method       BLASTX
NCBI GI      g1332411
BLAST score   270
E value      2.0e-24
Match length  56
% identity    91
NCBI Description (D85102) dihydroflavonol 4-reductase [Rosa hybrida]
```

```
Seq. No.      232387
Seq. ID      LIB3197-053-Q1-M1-F4
Method       BLASTX
NCBI GI      g417060
BLAST score   626
E. value     2.0e-65
Match length  121
% identity    94
NCBI Description  GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA
                  LIGASE) (GS) >gi 170637 (M94765) glutamine synthetase
```


NCBI Description (U89609) fiber annexin [*Gossypium hirsutum*]

```
Seq. No.      232393
Seq. ID      LIB3197-053-Q1-M1-G6
Method       BLASTX
NCBI GI      g2118231
BLAST score   578
E value      8.0e-60
Match length  149
% identity    79
NCBI Description H+-transporting ATPase (EC 3.6.1.35) AHA10 - Arabidopsis
thaliana >gi_765354_bbs_157347 (S74033) plasma membrane
H(+)-ATPase isoform AHA10=P-type ATPase [Arabidopsis
thaliana, cv. Columbia, Peptide, 946 aa] [Arabidopsis
thaliana]
```

```
Seq. No.      232394
Seq. ID      LIB3197-053-Q1-M1-H1
Method       BLASTX
NCBI GI      g3264759
BLAST score   562
E value      6.0e-58
Match length  127
% identity    87
NCBI Description (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
```

```
Seq. No.          232395
Seq. ID          LIB3197-053-Q1-M1-H11
Method           BLASTX
NCBI GI          g464846
BLAST score      645
E value          1.0e-67
Match length     145
% identity       86
NCBI Description  TUBULIN ALPHA-6 CHAIN >gi_322880_pir_S28983 tubulin
                  alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178)
                  alpha-tubulin #6 [Zea mays]
```

```
Seq. No.      232396
Seq. ID      LIB3197-053-Q1-M1-H12
Method       BLASTX
NCBI GI      g4262140
BLAST score   336
E value      2.0e-31
Match length  95
% identity    72
NCBI Description: (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]
```

```
Seq. No.      232397
Seq. ID      LIB3197-053-Q1-M1-H5
Method       BLASTX
NCBI GI      g2462741
BLAST score   281
E value       2.0e-42
Match length  136
% identity    65
NCBI Description (AC002292) Highly similar to auxin-induced protein
```


(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 232398
Seq. ID LIB3197-053-Q1-M1-H7
Method BLASTX
NCBI GI g1498053
BLAST score 122
E value 4.0e-13
Match length 87
% identity 56
NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 232399
Seq. ID LIB3197-054-Q1-M1-A10
Method BLASTX
NCBI GI g4103342
BLAST score 626
E value 2.0e-65
Match length 143
% identity 87
NCBI Description (AF022377) agamous-like putative transcription factor [Cucumis sativus]

Seq. No. 232400
Seq. ID LIB3197-054-Q1-M1-A4
Method BLASTX
NCBI GI g477226
BLAST score 287
E value 5.0e-26
Match length 69
% identity 90
NCBI Description heat shock protein HSP82 - maize >gi_300083_bbs_130886 (S59780) HSP82=82 kda heat shock protein [Zea mays, seedling, leaves, Peptide, 715 aa] [Zea mays]

Seq. No. 232401
Seq. ID LIB3197-054-Q1-M1-A6
Method BLASTX
NCBI GI g3875246
BLAST score 374
E value 7.0e-36
Match length 140
% identity 54
NCBI Description (Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene;

Seq. No. 232402
Seq. ID LIB3197-054-Q1-M1-A8
Method BLASTX
NCBI GI g3281868
BLAST score 540
E value 2.0e-55
Match length 121
% identity 81
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

NCBI GI g586076
 BLAST score 668
 E value 2.0e-70
 Match length 125
 % identity 98
 NCBI Description TUBULIN BETA-1 CHAIN >gi_486734_pir_S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No. 232409
 Seq. ID LIB3197-054-Q1-M1-B5
 Method BLASTX
 NCBI GI g1914683
 BLAST score 318
 E value 2.0e-29
 Match length 147
 % identity 51
 NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 232410
 Seq. ID LIB3197-054-Q1-M1-B6
 Method BLASTX
 NCBI GI g3914467
 BLAST score 142
 E value 1.0e-08
 Match length 90
 % identity 40
 NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum]

Seq. No. 232411
 Seq. ID LIB3197-054-Q1-M1-B7
 Method BLASTX
 NCBI GI g1771780
 BLAST score 526
 E value 9.0e-54
 Match length 132
 % identity 81
 NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 232412
 Seq. ID LIB3197-054-Q1-M1-C10
 Method BLASTX
 NCBI GI g4455192
 BLAST score 225
 E value 2.0e-18
 Match length 125
 % identity 42
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 232413
 Seq. ID LIB3197-054-Q1-M1-C11
 Method BLASTX
 NCBI GI g266463
 BLAST score 750
 E value 5.0e-80

E value	6.0e-43
Match length	93
% identity	95
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL9 >gi_2345158 (AF015552) AGL9 [Arabidopsis thaliana] >gi_2829878 (AC002396) AGL9 [Arabidopsis thaliana]
Seq. No.	232428
Seq. ID	LIB3197-054-Q1-M1-E2
Method	BLASTX
NCBI GI	g498038
BLAST score	612
E value	8.0e-64
Match length	146
% identity	80
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]
Seq. No.	232429
Seq. ID	LIB3197-054-Q1-M1-E4
Method	BLASTX
NCBI GI	g135535
BLAST score	439
E value	2.0e-43
Match length	97
% identity	91
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir_JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955 (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]
Seq. No.	232430
Seq. ID	LIB3197-054-Q1-M1-E5
Method	BLASTX
NCBI GI	g3218396
BLAST score	246
E value	7.0e-21
Match length	96
% identity	49
NCBI Description	(AL023860) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	232431
Seq. ID	LIB3197-054-Q1-M1-E6
Method	BLASTX
NCBI GI	g992706
BLAST score	566
E value	2.0e-58
Match length	110
% identity	92
NCBI Description	(U33758) UBC13 [Arabidopsis thaliana]
Seq. No.	232432
Seq. ID	LIB3197-054-Q1-M1-E8
Method	BLASTX
NCBI GI	g1658197
BLAST score	684

53

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Seq. No.      232469
Seq. ID      LIB3197-055-Q1-M1-F12
Method       BLASTX
NCBI GI      g2833389
BLAST score   617
E value      2.0e-64
Match length 138
% identity   79
NCBI Description SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III)
                >gi_1200154_emb_CAA65065_ (X95759) glycogen (starch)
                synthase [Solanum tuberosum]
```

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Seq. No.      232471
Seq. ID       LIB3197-055-Q1-M1-F6.
Method        BLASTX
NCBI GI       g729623
BLAST score   529
E value       4.0e-54
Match length  115
% identity    90
NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP
78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG
5) (BIP 5) >gi_100340_pir_S21880 heat shock protein BiP
homolog blp5 - common tobacco >gi_19813_emb_CAA42660_
(X60058) luminal binding protein (BiP) [Nicotiana tabacum]

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33493

Seq. ID LIB3197-055-Q1-M1-H6
Method BLASTX
NCBI GI g4469023
BLAST score 415
E value 7.0e-41
Match length 98
% identity 82
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 232484
Seq. ID LIB3197-055-Q1-M1-H7
Method BLASTX
NCBI GI g2494113
BLAST score 436
E value 3.0e-43
Match length 109
% identity 72
NCBI Description (AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No. 232485
Seq. ID LIB3197-055-Q1-M1-H8
Method BLASTX
NCBI GI g2498490
BLAST score 273
E value 4.0e-24
Match length 109
% identity 46
NCBI Description VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556) Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi_4503521_ref_NP_001559.1_pEIF3S6 murine mammary tumor integration site 6 (oncogene homolog)

Seq. No. 232486
Seq. ID LIB3197-055-Q1-M1-H9
Method BLASTX
NCBI GI g2062167
BLAST score 203
E value 5.0e-16
Match length 69
% identity 65
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 232487
Seq. ID LIB3197-056-Q1-M1-A10
Method BLASTX
NCBI GI g3548803
BLAST score 573
E value 2.0e-59
Match length 126
% identity 87
NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis

NCBI GI g1170898
 BLAST score. 322
 E value 4.0e-30
 Match length 92
 % identity 78
 NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
 >gi_629659_pir_S44167 malate dehydrogenase, mitochondrial
 - cider tree >gi_473206_emb_CAA55383_ (X78800)
 mitochondrial malate dehydrogenase [Eucalyptus gunnii]

Seq. No. 232493
 Seq. ID LIB3197-056-Q1-M1-A9
 Method BLASTX
 NCBI GI g2811278
 BLAST score 434
 E value 8.0e-43
 Match length 122
 % identity 74
 NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 232494
 Seq. ID LIB3197-056-Q1-M1-B1
 Method BLASTX
 NCBI GI g2463509
 BLAST score 442
 E value 3.0e-44
 Match length 89
 % identity 89
 NCBI Description (Y09541) pectate lyase [Zinnia elegans]

Seq. No. 232495
 Seq. ID LIB3197-056-Q1-M1-B10
 Method BLASTX
 NCBI GI g2811278
 BLAST score 637
 E value 9.0e-67
 Match length 130
 % identity 88
 NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 232496
 Seq. ID LIB3197-056-Q1-M1-B11
 Method BLASTX
 NCBI GI g1890317
 BLAST score 262
 E value 5.0e-23
 Match length 60
 % identity 78
 NCBI Description (Y11791) peroxidase ATP26a [Arabidopsis thaliana]

Seq. No. 232497
 Seq. ID LIB3197-056-Q1-M1-B12
 Method BLASTX
 NCBI GI g1351303
 BLAST score 245
 E value 6.0e-21
 Match length 62

% identity	61
NCBI Description	(X92491) TOM20 [Solanum tuberosum]
Seq. No.	232503
Seq. ID	LIB3197-056-Q1-M1-C2
Method	BLASTX
NCBI GI	g643469
BLAST score	398
E value	9.0e-39
Match length	138
% identity	57
NCBI Description	(U19886) unknown [Lycopersicon esculentum]
Seq. No.	232504
Seq. ID	LIB3197-056-Q1-M1-C3
Method	BLASTX
NCBI GI	g2213425
BLAST score	512
E value	3.0e-52
Match length	109
% identity	51
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]
Seq. No.	232505
Seq. ID	LIB3197-056-Q1-M1-C4
Method	BLASTX
NCBI GI	g2213425
BLAST score	179
E value	3.0e-17
Match length	64
% identity	41
NCBI Description	(Z97064) hypothetical protein [Citrus x paradisi]
Seq. No.	232506
Seq. ID	LIB3197-056-Q1-M1-C5
Method	BLASTX
NCBI GI	g1181333
BLAST score	184
E value	1.0e-13
Match length	40
% identity	78
NCBI Description	(X78057) calreticulin [Zea mays]
Seq. No.	232507
Seq. ID	LIB3197-056-Q1-M1-C8
Method	BLASTX
NCBI GI	g1076746
BLAST score	289
E value	9.0e-37
Match length	99
% identity	76
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]
Seq. No.	232508
Seq. ID	LIB3197-056-Q1-M1-C9


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NCBI GI                g267079
BLAST score            276
E value                2.0e-24
Match length          52
% identity             100
NCBI Description       TUBULIN BETA-6 CHAIN >gi_320187_pir_JQ1590 tubulin beta-6
                      chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6
                      tubulin [Arabidopsis thaliana]

Seq. No.              232530
Seq. ID               LIB3197-056-Q1-M1-G1
Method                BLASTX
NCBI GI               g2507281
BLAST score           571
E value               5.0e-59
Match length          104
% identity            100
NCBI Description       GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
                      (X97380) atran2 [Arabidopsis thaliana]

Seq. No.              232531
Seq. ID               LIB3197-056-Q1-M1-G3
Method                BLASTX
NCBI GI               g267069
BLAST score           515
E value               2.0e-52
Match length          95
% identity             99
NCBI Description       TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594
                      tubulin alpha chain - Arabidopsis thaliana >gi_166914
                      (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                      (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.              232532
Seq. ID               LIB3197-056-Q1-M1-G7
Method                BLASTX
NCBI GI               g3914996
BLAST score           160
E value               4.0e-11
Match length          78
% identity             51
NCBI Description       PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
                      >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine
                      aminotransferase [Arabidopsis thaliana]
                      >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine
                      aminotransferase [Arabidopsis thaliana]
                      >gi_3367581_emb_CAA20033_ (AL031135) phosphoserine
                      aminotransferase [Arabidopsis thaliana]

Seq. No.              232533
Seq. ID               LIB3197-056-Q1-M1-G8
Method                BLASTX
NCBI GI               g267069
BLAST score           437
E value               2.0e-43
Match length          86
% identity             94

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NCBI GI             g4097579
BLAST score         565
E value             2.0e-58
Match length        117
% identity          86
NCBI Description     (U64922) NTGP1 [Nicotiana tabacum]

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Seq. No.      232544
Seq. ID      LIB3197-057-Q1-M1-A7
Method       BLASTX
NCBI GI      g232029
BLAST score   144
E value      7.0e-13
Match length  119
% identity    42
NCBI Description  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                >gi_100154_pir_S21989 translation elongation factor eEF-1
                alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)
                elongation factor 1A [Daucus carota]
```

```
Seq. No.      232546
Seq. ID       LIB3197-057-Q1-M1-A9
Method        BLASTX
NCBI GI       g1076660
BLAST score   380
E value       1.0e-36
Match length  104
% identity    74
NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122
                (S74753) MybSt1=Myb-related transcriptional activator
                {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                leaf, Peptide, 342 aa] [Solanum tuberosum]
```

```
Seq. No.      232548
Seq. ID      LIB3197-057-Q1-M1-B11
Method       BLASTX
```


BLAST score	350
E value	4.0e-33
Match length	89
% identity	78
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	232559
Seq. ID	LIB3197-057-Q1-M1-D11
Method	BLASTX
NCBI GI	g3047085
BLAST score	447
E value	2.0e-44
Match length	132
% identity	66
NCBI Description	(AF058914) No definition line found [Arabidopsis thaliana]
Seq. No.	232560
Seq. ID	LIB3197-057-Q1-M1-D12
Method	BLASTX
NCBI GI	g4490330
BLAST score	744
E value	3.0e-79
Match length	144
% identity	94
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]
Seq. No.	232561
Seq. ID	LIB3197-057-Q1-M1-D2
Method	BLASTX
NCBI GI	g4580394
BLAST score	267
E value	2.0e-23
Match length	123
% identity	42
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]
Seq. No.	232562
Seq. ID	LIB3197-057-Q1-M1-D4
Method	BLASTX
NCBI GI	g2462827
BLAST score	220
E value	5.0e-18
Match length	64
% identity	70
NCBI Description	(AF000657) probable thiamin biosynthetic enzyme [Arabidopsis thaliana]
Seq. No.	232563
Seq. ID	LIB3197-057-Q1-M1-D8
Method	BLASTX
NCBI GI	g2062167
BLAST score	442
E value	7.0e-44
Match length	102
% identity	80

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
(CCT-ALPHA) >gi_322602_pir_JN0448 t-complex polypeptide
Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_
(D11351) t-complex polypeptide 1 homologue [Arabidopsis
thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 232590
Seq. ID LIB3197-057-Q1-M1-H6
Method BLASTX
NCBI GI g1931647
BLAST score 320
E value 1.0e-29
Match length 86
% identity 71
NCBI Description (U95973) endomembrane protein EMP70 precursor isolog
[Arabidopsis thaliana]

Seq. No. 232591
Seq. ID LIB3197-057-Q1-M1-H8
Method BLASTX
NCBI GI g3687237
BLAST score 227
E value 7.0e-19
Match length 100
% identity 53
NCBI Description (AC005169) putative Cys3His zinc-finger protein
[Arabidopsis thaliana]

Seq. No. 232592
Seq. ID LIB3197-058-Q1-M1-B1
Method BLASTX
NCBI GI g1663706
BLAST score 192
E value 1.0e-14
Match length 92
% identity 47
NCBI Description (D87685) similar to human transcription factor TFIIS
(S34159). [Homo sapiens]

Seq. No. 232593
Seq. ID LIB3197-058-Q1-M1-B2
Method BLASTX
NCBI GI g4220476
BLAST score 200
E value 2.0e-16
Match length 87
% identity 60
NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No. 232594
Seq. ID LIB3197-058-Q1-M1-C3
Method BLASTX
NCBI GI g3025299
BLAST score 149
E value 2.0e-09
Match length 116

09684016-101000

```
% identity      31
NCBI Description HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660
                  (AF002109) ABC1 isolog [Arabidopsis thaliana]

Seq. No.        232595
Seq. ID         LIB3197-058-Q1-M1-C7
Method          BLASTX
NCBI GI         g113116
BLAST score     391
E value         6.0e-38
Match length    140
% identity      52
NCBI Description ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
                  >gi_111396_pir_A35007 ATP citrate (pro-S)-lyase (EC
                  4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
                  [Rattus norvegicus]

Seq. No.        232596
Seq. ID         LIB3197-058-Q1-M1-D1
Method          BLASTX
NCBI GI         g3193284
BLAST score     235
E value         9.0e-20
Match length    116
% identity      37
NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.        232597
Seq. ID         LIB3197-058-Q1-M1-D2
Method          BLASTX
NCBI GI         g4559310
BLAST score     151
E value         8.0e-10
Match length    133
% identity      29
NCBI Description (AF129131) putative Zic3 binding protein; CBP3 protein
                  homolog [Xenopus laevis]

Seq. No.        232598
Seq. ID         LIB3197-058-Q1-M1-D3
Method          BLASTX
NCBI GI         g3702962
BLAST score     309
E value         3.0e-28
Match length    61
% identity      95
NCBI Description (AF079484) rac GTP binding protein Arac7 [Arabidopsis
                  thaliana]

Seq. No.        232599
Seq. ID         LIB3197-058-Q1-M1-D9
Method          BLASTX
NCBI GI         g2444178
BLAST score     689
E value         7.0e-73
Match length    140
% identity      91
```


NCBI Description (U94784) unconventional myosin [Helianthus annuus]

Seq. No. 232600
Seq. ID LIB3197-058-Q1-M1-E9
Method BLASTX
NCBI GI g125887
BLAST score 110
E value 1.0e-09
Match length 86
% identity 49
NCBI Description ANTHR SPECIFIC LAT52 PROTEIN PRECURSOR
>gi_82092_pir_S04765 LAT52 protein precursor - tomato
>gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
esculentum]

Seq. No. 232601
Seq. ID LIB3197-058-Q1-M1-F1
Method BLASTX
NCBI GI g1174592
BLAST score 548
E value 2.0e-56
Match length 120
% identity 86
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
- garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
sativum]

Seq. No. 232602
Seq. ID LIB3197-058-Q1-M1-F7
Method BLASTX
NCBI GI g4337175
BLAST score 433
E value 7.0e-43
Match length 123
% identity 67
NCBI Description (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 232603
Seq. ID LIB3197-058-Q1-M1-F8
Method BLASTX
NCBI GI g972511
BLAST score 141
E value 1.0e-18
Match length 60
% identity 87
NCBI Description (X90982) phosphoenolpyruvate carboxylase [Solanum
tuberosum]

Seq. No. 232604
Seq. ID LIB3197-058-Q1-M1-G1
Method BLASTX
NCBI GI g1354849
BLAST score 293
E value 9.0e-33

Match length	131
% identity	42
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]
Seq. No.	232605
Seq. ID	LIB3197-058-Q1-M1-G2
Method	BLASTX
NCBI GI	g1351014
BLAST score	461
E value	3.0e-46
Match length	111
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]
Seq. No.	232606
Seq. ID	LIB3197-058-Q1-M1-G7
Method	BLASTX
NCBI GI	g1486472
BLAST score	372
E value	1.0e-35
Match length	91
% identity	78
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]
Seq. No.	232607
Seq. ID	LIB3197-058-Q1-M1-G9
Method	BLASTX
NCBI GI	g3128175
BLAST score	144
E value	6.0e-09
Match length	90
% identity	37
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.	232608
Seq. ID	LIB3197-058-Q1-M1-H1
Method	BLASTX
NCBI GI	g461736
BLAST score	560
E value	8.0e-58
Match length	118
% identity	95
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_478786_pir_S29316 chaperonin 60 - cucurbit >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita sp.]
Seq. No.	232609
Seq. ID	LIB3197-058-Q1-M1-H3
Method	BLASTX
NCBI GI	g2245132
BLAST score	187
E value	5.0e-14
Match length	69
% identity	58

Seq. No.	232620
Seq. ID	LIB3197-059-Q1-M1-B1
Method	BLASTX
NCBI GI	g3643598
BLAST score	657
E value	4.0e-69
Match length	146
% identity	84
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]
Seq. No.	232621
Seq. ID	LIB3197-059-Q1-M1-B4
Method	BLASTX
NCBI GI	g4567250
BLAST score	196
E value	5.0e-15
Match length	86
% identity	55
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.	232622
Seq. ID	LIB3197-059-Q1-M1-B7
Method	BLASTX
NCBI GI	g3319355
BLAST score	535
E value	7.0e-55
Match length	125
% identity	91
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]
Seq. No.	232623
Seq. ID	LIB3197-059-Q1-M1-B8
Method	BLASTX
NCBI GI	g4432845
BLAST score	158
E value	1.0e-10
Match length	85
% identity	45
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.	232624
Seq. ID	LIB3197-059-Q1-M1-B9
Method	BLASTX
NCBI GI	g584867
BLAST score	166
E value	1.0e-11
Match length	113
% identity	33
NCBI Description	CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5) >gi_481959_pir_S40266 gene CYP77A2 protein - eggplant >gi_542071_pir_S41598 cytochrome P450 77A2 - eggplant >gi_438241_emb_CAA50646_ (X71655) CYP77A2 [Solanum melongena]

(AJ222771) T protein [Pisum sativum]

Seq. No. 232640
 Seq. ID LIB3197-059-Q1-M1-G1
 Method BLASTX
 NCBI GI g2288981
 BLAST score 300
 E value 3.0e-27
 Match length 89
 % identity 39
 NCBI Description (AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi 3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No. 232641
 Seq. ID LIB3197-059-Q1-M1-G11
 Method BLASTX
 NCBI GI g3702332
 BLAST score 251
 E value 1.0e-21
 Match length 81
 % identity 58
 NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 232642
 Seq. ID LIB3197-059-Q1-M1-G12
 Method BLASTX
 NCBI GI g3738297
 BLAST score 271
 E value 7.0e-24
 Match length 92
 % identity 28
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 232643
 Seq. ID LIB3197-059-Q1-M1-G3
 Method BLASTX
 NCBI GI g1477428
 BLAST score 615
 E value 3.0e-64
 Match length 140
 % identity 85
 NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 232644
 Seq. ID LIB3197-059-Q1-M1-G5
 Method BLASTX
 NCBI GI g3063710
 BLAST score 498
 E value 2.0e-50
 Match length 144
 % identity 66
 NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 232645
 Seq. ID LIB3197-059-Q1-M1-G6
 Method BLASTX

NCBI Description tubulin beta-1 chain - rice

Seq. No. 232656
Seq. ID LIB3197-059-Q1-M1-H9
Method BLASTX
NCBI GI g3169287
BLAST score 166
E value 1.0e-11
Match length 52
% identity 65

NCBI Description (AF050673) vacuolar H⁺-ATPase catalytic subunit [Gossypium hirsutum]

Seq. No. 232657
Seq. ID LIB3197-060-Q1-M1-A10
Method BLASTX
NCBI GI g1172872
BLAST score 310
E value 2.0e-28
Match length 132
% identity 56

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir_JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 232658
Seq. ID LIB3197-060-Q1-M1-A11
Method BLASTX
NCBI GI g1076746
BLAST score 652
E value 3.0e-69
Match length 147
% identity 97

NCBI Description heat shock protein 70 - rice (fragment)
>gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No. 232659
Seq. ID LIB3197-060-Q1-M1-A2
Method BLASTX
NCBI GI g586076
BLAST score 528
E value 5.0e-54
Match length 105
% identity 88

NCBI Description TUBULIN BETA-1 CHAIN >gi_486734_pir_S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta tubulin 1 [Lupinus albus]

Seq. No. 232660
Seq. ID LIB3197-060-Q1-M1-A3
Method BLASTX
NCBI GI g1172872
BLAST score 264

BLAST score 241
 E value 2.0e-20
 Match length 55
 % identity 67
 NCBI Description (AC005396) gibberellin-regulated protein GAST1-like
 [Arabidopsis thaliana]

Seq. No. 232666
 Seq. ID LIB3197-060-Q1-M1-B5
 Method BLASTX
 NCBI GI g2384671
 BLAST score 578
 E value 8.0e-60
 Match length 150
 % identity 74
 NCBI Description (AF012657) putative potassium transporter AtKT2p
 [Arabidopsis thaliana]

Seq. No. 232667
 Seq. ID LIB3197-060-Q1-M1-B7
 Method BLASTX
 NCBI GI g1245343
 BLAST score 226
 E value 1.0e-18
 Match length 65
 % identity 62
 NCBI Description (U50194) tripeptidylpeptidase II [Rattus norvegicus]

Seq. No. 232668
 Seq. ID LIB3197-060-Q1-M1-B8
 Method BLASTX
 NCBI GI g1777921
 BLAST score 615
 E value 3.0e-64
 Match length 126
 % identity 93
 NCBI Description (U54774) glutamate decarboxylase [Nicotiana tabacum]

Seq. No. 232669
 Seq. ID LIB3197-060-Q1-M1-C10
 Method BLASTX
 NCBI GI g2832625
 BLAST score 431
 E value 1.0e-42
 Match length 102
 % identity 81
 NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 232670
 Seq. ID LIB3197-060-Q1-M1-C11
 Method BLASTX
 NCBI GI g3023271
 BLAST score 691
 E value 4.0e-73
 Match length 140
 % identity 95
 NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)

(FALDH) (GSH-FDH) >gi_1675394 (U77637) class III ADH enzyme
[Oryza sativa]

Seq. No. 232671
Seq. ID LIB3197-060-Q1-M1-C2
Method BLASTX
NCBI GI g3334115
BLAST score 546
E value 4.0e-56
Match length 110
% identity 97
NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
(AF006489) adenine nucleotide translocator 1 [Gossypium
hirsutum]

Seq. No. 232672
Seq. ID LIB3197-060-Q1-M1-C3
Method BLASTX
NCBI GI g507275
BLAST score 178
E value 5.0e-13
Match length 105
% identity 40
NCBI Description (L34159) NADPH:quinone oxidoreductase/zeta crystallin [Lama
guanicoe]

Seq. No. 232673
Seq. ID LIB3197-060-Q1-M1-C5
Method BLASTX
NCBI GI g3269293
BLAST score 275
E value 3.0e-24
Match length 132
% identity 47
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 232674
Seq. ID LIB3197-060-Q1-M1-C6
Method BLASTX
NCBI GI g1771162
BLAST score 515
E value 2.0e-52
Match length 130
% identity 82
NCBI Description (X98930) SBT2 [Lycopersicon esculentum]
>gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like
protease [Lycopersicon esculentum]

Seq. No. 232675
Seq. ID LIB3197-060-Q1-M1-C7
Method BLASTX
NCBI GI g1170567
BLAST score 635
E value 2.0e-67
Match length 143
% identity 92


```

Method          BLASTX
NCBI GI         4974782
BLAST score     493
E value         5.0e-50
Match length    99
% identity      99
NCBI Description (Z49150) cobalamine-independent methionine synthase
[Solenostemon scutellarioides]

```

```
Seq. No.      232687
Seq. ID      LIB3197-060-Q1-M1-E1
Method       BLASTX
NCBI GI      g2459420
BLAST score   638
E value      6.0e-67
Match length  125
% identity    97
NCBI Description (AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]
```

```
Seq. No.      232688
Seq. ID      LIB3197-060-Q1-M1-E10
Method       BLASTX
NCBI GI      g3859659
BLAST score   151
E value      9.0e-10
Match length  60
% identity    53
NCBI Description (AL031394) putative potassium transporter AtKT5p (AtKT5)
               [Arabidopsis thaliana].
```

```
Seq. No.      232689
Seq. ID       LIB3197-060-Q1-M1-E11
Method        BLASTX
NCBI GI       g1491615
BLAST score    252
E value       1.0e-21
Match length   113
% identity     45
NCBI Description (X99923) male sterility 2-like protein [Arabidopsis thaliana]
```

```

Seq. No.          232690
Seq. ID           LIB3197-060-Q1-M1-E2
Method            BLASTX
NCBI GI           g3023815
BLAST score       370
E value           2.0e-35
Match length      108
% identity        69
NCBI Description   GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
                   (G6PD) >gi_1362053_pir_S57785 glucose-6-phosphate
                   1-dehydrogenase (EC 1.1.1.49) - alfalfa >gi_603219 (U18238)
                   glucose-6-phosphate dehydrogenase [Medicago sativa subsp.
                   sativa]

```

Seq. No. 232691


```
Seq. ID          LIB3197-060-Q1-M1-E3
Method           BLASTX
NCBI GI          g2497492
BLAST score      240
E value          9.0e-26
Match length     121
% identity       55
NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
                  KINASE) >gi_1653646_dbj_BAA18558_ (D90915) uridine
                  monophosphate kinase [Synechocystis sp.]
```

```
Seq. No.      232692
Seq. ID       LIB3197-060-Q1-M1-E6
Method        BLASTX
NCBI GI       g2129578
BLAST score    227
E value        8.0e-19
Match length   63
% identity     75
NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
                  thaliana >gi_928932_emb_CAA89205_(Z49239) homolog of
                  dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                  >gi_1585435_prf_2124427B diamide resistance gene
                  [Arabidopsis thaliana]
```

```
Seq. No.      232693
Seq. ID      LIB3197-060-Q1-M1-E7
Method       BLASTX
NCBI GI      g2880051
BLAST score   167
E value      1.0e-11
Match length  64
% identity   53
NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]
```

```
Seq. No.      232694
Seq. ID      LIB3197-060-Q1-M1-E8
Method       BLASTX
NCBI GI      g134891
BLAST score   142
E value      9.0e-09
Match length  99
% identity    35
NCBI Description  SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
                (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                >gi_89066_pir_A24570 signal recognition particle receptor
                precursor - dog >gi_997_emb_CAA26945_ (X03184) signal
                recognition particle receptor [Canis sp.]
                >gi_224778_prf_1112224A signal recognition particle
                receptor [Canis familiaris]
```

```
Seq. No.      232695
Seq. ID      LIB3197-060-Q1-M1-F12
Method       BLASTX
NCBI GI      g484656
BLAST score   599
E value      3.0e-62
```



```
Seq. ID      LIB3197-060-Q1-M1-G9
Method       BLASTX
NCBI GI      g267069
BLAST score   616
E value      3.0e-64
Match length  114
% identity    99
NCBI Description  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
```

```
Seq. No.      232707
Seq. ID       LIB3197-060-Q1-M1-H1
Method        BLASTX
NCBI GI       g4539408
BLAST score   287
E value       1.0e-25
Match length   74
% identity     73
NCBI Description (AL049524) putative alpha NAC [Arabidopsis thaliana]
```

```
Seq. No.      232708
Seq. ID       LIB3197-060-Q1-M1-H10
Method        BLASTX
NCBI GI       g4512671
BLAST score   299
E value       4.0e-27
Match length  74
% identity    73
NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      232709
Seq. ID      LIB3197-060-Q1-M1-H11
Method       BLASTX
NCBI GI      g3041738
BLAST score   431
E value      1.0e-42
Match length  146
% identity    60
NCBI Description  T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
                (HIV-1 NEF INTERACTING PROTEIN) >gi_2559010 (AF026292)
                chaperonin containing t-complex polypeptide 1, eta subunit;
                CCT-eta [Homo sapiens]
```

```
Seq. No.      232710
Seq. ID      LIB3197-060-Q1-M1-H6
Method       BLASTX
NCBI GI      g2118222
BLAST score   364
E value      9.0e-35
Match length  87
% identity    54
NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                (clone AVA-P4) - Arabidopsis thaliana >gi_926935 (L44584)
                vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                thaliana]
```


NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 232721
 Seq. ID LIB3272-001-P1-K1-B3
 Method BLASTX
 NCBI GI g3522952
 BLAST score 424
 E value 8.0e-42
 Match length 125
 % identity 66

NCBI Description (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 232722
 Seq. ID LIB3272-001-P1-K1-B4
 Method BLASTX
 NCBI GI g529353
 BLAST score 295
 E value 1.0e-26
 Match length 101
 % identity 54

NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 232723
 Seq. ID LIB3272-001-P1-K1-B8
 Method BLASTX
 NCBI GI g2662343
 BLAST score 566
 E value 2.0e-58
 Match length 112
 % identity 96

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 232724
 Seq. ID LIB3272-001-P1-K1-B9
 Method BLASTX
 NCBI GI g3395430
 BLAST score 144
 E value 5.0e-09
 Match length 115
 % identity 34

NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 232725
 Seq. ID LIB3272-001-P1-K1-C1
 Method BLASTX
 NCBI GI g832876
 BLAST score 553
 E value 6.0e-57
 Match length 120
 % identity 90

NCBI Description (L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf_2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No. 232726
 Seq. ID LIB3272-001-P1-K1-C10

BLAST score 219
E value 9.0e-18
Match length 131
% identity 42
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 232732
Seq. ID LIB3272-001-P1-K1-C8
Method BLASTX
NCBI GI g2984709
BLAST score 442
E value 6.0e-44
Match length 91
% identity 90
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 232733
Seq. ID LIB3272-001-P1-K1-D1
Method BLASTX
NCBI GI g4539386
BLAST score 311
E value 1.0e-28
Match length 134
% identity 25
NCBI Description (AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No. 232734
Seq. ID LIB3272-001-P1-K1-D11
Method BLASTX
NCBI GI g3869088
BLAST score 570
E value 6.0e-59
Match length 109
% identity 100
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 232735
Seq. ID LIB3272-001-P1-K1-D3
Method BLASTX
NCBI GI g3420051
BLAST score 611
E value 1.0e-63
Match length 110
% identity 96
NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

Seq. No. 232736
Seq. ID LIB3272-001-P1-K1-D4
Method BLASTX
NCBI GI g1172955
BLAST score 210
E value 1.0e-16
Match length 66
% identity 59
NCBI Description 50S RIBOSOMAL PROTEIN L13 >gi_1075232_pir_G64123 ribosomal protein L13 (rpL13) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1574283 (U32823) ribosomal protein L13

Described in: 10.1000

```
Seq. No.      232738
Seq. ID      LIB3272-001-P1-K1-D6
Method       BLASTX
NCBI GI      g4567307
BLAST score   207
E value      2.0e-16
Match length 102
% identity    45
NCBI Description (AC005956) putative zinc finger protein [Arabidopsis thaliana]
```

```
Seq. No.      232739
Seq. ID      LIB3272-001-P1-K1-D7
Method       BLASTX
NCBI GI      g131772
BLAST score   288
E value      7.0e-26
Match length  74
% identity    81
NCBI Description  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
                >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                maize
```

```
Seq. No.          232740
Seq. ID           LIB3272-001-P1-K1-D9
Method            BLASTX
NCBI GI           g3915873
BLAST score       714
E value           8.0e-76
Match length      136
% identity        96
NCBI Description   SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
                   (NODULIN-100) >gi_2606081 (AF030231) sucrose synthase
                   [Glycine max]
```

```
Seq. No.      232741
Seq. ID       LIB3272-001-P1-K1-E1
Method        BLASTX
NCBI GI       g3063396
BLAST score    525
E value       1.0e-53
Match length   118
% identity     84
NCBI Description (AB012947) vcCyp [Vicia faba]
```


Seq. ID LIB3272-001-P1-K1-E6
 Method BLASTX
 NCBI GI g4510346
 BLAST score 168
 E value 8.0e-12
 Match length 38
 % identity 87
 NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 232748
 Seq. ID LIB3272-001-P1-K1-E7
 Method BLASTX
 NCBI GI g3868758
 BLAST score 445
 E value 3.0e-44
 Match length 108
 % identity 75
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 232749
 Seq. ID LIB3272-001-P1-K1-E9
 Method BLASTX
 NCBI GI g1174592
 BLAST score 713
 E value 1.0e-75
 Match length 135
 % identity 98
 NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
 - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
 sativum]

Seq. No. 232750
 Seq. ID LIB3272-001-P1-K1-F1
 Method BLASTX
 NCBI GI g4337046
 BLAST score 308
 E value 3.0e-28
 Match length 118
 % identity 57
 NCBI Description (AF124162) molybdopterin synthase sulphurylase [Nicotiana
 plumbaginifolia]

Seq. No. 232751
 Seq. ID LIB3272-001-P1-K1-F11
 Method BLASTX
 NCBI GI g3420239
 BLAST score 333
 E value 3.0e-31
 Match length 63
 % identity 100
 NCBI Description (AF059484) actin [Gossypium hirsutum]

Seq. No. 232752
 Seq. ID LIB3272-001-P1-K1-F12
 Method BLASTX
 NCBI GI g4455323
 BLAST score 356

09684016-101000

Seq. No. 232763
Seq. ID LIB3272-001-P1-K1-G6
Method BLASTX
NCBI GI g267082
BLAST score 632
E value 3.0e-66
Match length 118
% identity 98
NCBI Description TUBULIN BETA-8 CHAIN >gi_320189_pir_JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No. 232764
Seq. ID LIB3272-001-P1-K1-G7
Method BLASTX
NCBI GI g3878594
BLAST score 109
E value 3.0e-10
Match length 106
% identity 34
NCBI Description (Z81102) Similarity to Mouse CMP-sialic acid transporter (TR:Q61420) [Caenorhabditis elegans]
>gi_3881872_emb_CAB05329_ (Z82288) Similarity to Mouse CMP-sialic acid transporter (TR:Q61420) [Caenorhabditis elegans]

Seq. No. 232765
Seq. ID LIB3272-001-P1-K1-G8
Method BLASTX
NCBI GI g2493131
BLAST score 503
E value 4.0e-51
Match length 106
% identity 95
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit [Hordeum vulgare]

Seq. No. 232766
Seq. ID LIB3272-001-P1-K1-G9
Method BLASTX
NCBI GI g3901014
BLAST score 235
E value 1.0e-19
Match length 55
% identity 76
NCBI Description (AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No. 232767
Seq. ID LIB3272-001-P1-K1-H10
Method BLASTX
NCBI GI g4521249
BLAST score 442
E value 6.0e-44
Match length 111

% identity	73
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]
Seq. No.	232784
Seq. ID	LIB3272-002-P1-K1-B5
Method	BLASTX
NCBI GI	g4056502
BLAST score	432
E value	9.0e-43
Match length	103
% identity	83
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.	232785
Seq. ID	LIB3272-002-P1-K1-B7
Method	BLASTX
NCBI GI	g1173256
BLAST score	633
E value	3.0e-66
Match length	123
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882_ (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]
Seq. No.	232786
Seq. ID	LIB3272-002-P1-K1-C10
Method	BLASTX
NCBI GI	g2160166
BLAST score	466
E value	9.0e-47
Match length	135
% identity	62
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.	232787
Seq. ID	LIB3272-002-P1-K1-C12
Method	BLASTX
NCBI GI	g2351380
BLAST score	235
E value	1.0e-19
Match length	96
% identity	54
NCBI Description	(U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens] >gi_4503515_ref_NP_003747.1_pEIF3S3_ UNKNOWN
Seq. No.	232788
Seq. ID	LIB3272-002-P1-K1-C5
Method	BLASTX
NCBI GI	g1326338
BLAST score	178
E value	4.0e-13
Match length	85
% identity	46
NCBI Description	(U58746) R05G6.4 gene product [Caenorhabditis elegans]

Seq. No.	232789
Seq. ID	LIB3272-002-P1-K1-C8
Method	BLASTX
NCBI GI	g4538905
BLAST score	585
E value	1.0e-60
Match length	132
% identity	83
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

```
Seq. No.      232790
Seq. ID      LIB3272-002-P1-K1-C9
Method       BLASTX
NCBI GI      g2827558
BLAST score   159
E value      1.0e-10
Match length  53
% identity    53
NCBI Description (AL021635) putative DNA binding protein [Arabidopsis
thaliana]
```

```
Seq. No.          232791
Seq. ID           LIB3272-002-P1-K1-D1
Method            BLASTX
NCBI GI           g2213590
BLAST score       186
E value           6.0e-14
Match length      78
% identity        41
NCBI Description   (AC000348) T7N9.10 [Arabidopsis thaliana]
```

```
Seq. No.      232792
Seq. ID       LIB3272-002-P1-K1-D10
Method        BLASTX
NCBI GI       g4455208
BLAST score    555
E value        3.0e-57
Match length   134
% identity     81
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      232793
Seq. ID       LIB3272-002-P1-K1-D11
Method        BLASTX
NCBI GI       g4204303
BLAST score   596
E value       5.0e-62
Match length  129
% identity    82
NCBI Description (AC003027) lcl_prt_seq No definition line found
                [Arabidopsis thaliana]
```

```
Seq. No.      232794
Seq. ID      LIB3272-002-P1-K1-D12
Method       BLASTX
NCBI GI      g3023815
BLAST score  516
```


E value	2.0e-45
Match length	136
% identity	65
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_2129912_pir_S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi_1184668 (U22147) beta-1,3-glucanase [Hevea brasiliensis]
Seq. No.	232810
Seq. ID	LIB3272-002-P1-K1-F2
Method	BLASTX
NCBI GI	g3913633
BLAST score	363
E value	1.0e-34
Match length	113
% identity	66
NCBI Description	HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown protein [Arabidopsis thaliana]
Seq. No.	232811
Seq. ID	LIB3272-002-P1-K1-F3
Method	BLASTX
NCBI GI	g2501647
BLAST score	476
E value	6.0e-48
Match length	127
% identity	75
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi_1362120_pir_S55732 uroporphyrinogen decarboxylase - common tobacco >gi_1009429_emb_CAA58040_ (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]
Seq. No.	232812
Seq. ID	LIB3272-002-P1-K1-F4
Method	BLASTX
NCBI GI	g2244806
BLAST score	257
E value	3.0e-22
Match length	92
% identity	55
NCBI Description	(297336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	232813
Seq. ID	LIB3272-002-P1-K1-F5
Method	BLASTX
NCBI GI	g549063
BLAST score	506
E value	2.0e-51
Match length	117
% identity	82
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	232814
Seq. ID	LIB3272-002-P1-K1-F7
Method	BLASTX
NCBI GI	g3158376
BLAST score	473
E value	1.0e-47
Match length	125
% identity	76
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]
Seq. No.	232815
Seq. ID	LIB3272-002-P1-K1-F8
Method	BLASTX
NCBI GI	g1917019
BLAST score	549
E value	2.0e-56
Match length	114
% identity	90
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]
Seq. No.	232816
Seq. ID	LIB3272-002-P1-K1-F9
Method	BLASTX
NCBI GI	g2911362
BLAST score	245
E value	1.0e-22
Match length	118
% identity	58
NCBI Description	(AF041045) NADPH HC toxin reductase [Zea mays]
Seq. No.	232817
Seq. ID	LIB3272-002-P1-K1-G1
Method	BLASTX
NCBI GI	g3694872
BLAST score	461
E value	4.0e-46
Match length	112
% identity	78
NCBI Description	(AF092547) profilin [Ricinus communis]
Seq. No.	232818
Seq. ID	LIB3272-002-P1-K1-G10
Method	BLASTX
NCBI GI	g3668089
BLAST score	217
E value	1.0e-17
Match length	80
% identity	47
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	232819
Seq. ID	LIB3272-002-P1-K1-G11
Method	BLASTX
NCBI GI	g2662343
BLAST score	601
E value	1.0e-62
Match length	117

% identity	85
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus vulgaris]
Seq. No.	232825
Seq. ID	LIB3272-002-P1-K1-H10
Method	BLASTX
NCBI GI	g3668089
BLAST score	182
E value	2.0e-13
Match length	86
% identity	42
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.	232826
Seq. ID	LIB3272-002-P1-K1-H11
Method	BLASTX
NCBI GI	g120669
BLAST score	484
E value	6.0e-49
Match length	120
% identity	78
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.	232827
Seq. ID	LIB3272-002-P1-K1-H12
Method	BLASTX
NCBI GI	g4454097
BLAST score	273
E value	4.0e-24
Match length	66
% identity	82
NCBI Description	(X85206) hybrid proline-rich protein [Catharanthus roseus]
Seq. No.	232828
Seq. ID	LIB3272-002-P1-K1-H2
Method	BLASTX
NCBI GI	g1169782
BLAST score	255
E value	5.0e-22
Match length	101
% identity	57
NCBI Description	FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]
Seq. No.	232829
Seq. ID	LIB3272-002-P1-K1-H3
Method	BLASTX
NCBI GI	g1170747
BLAST score	296
E value	8.0e-27
Match length	72

% identity 82
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345.
(M88324) late embryogenesis-abundant protein [Gossypium
hirsutum] >gi_167347 (M37697) Lea5-A late
embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 232830
Seq. ID LIB3272-002-P1-K1-H4
Method BLASTX
NCBI GI g2160166
BLAST score 469
E value 4.0e-47
Match length 128
% identity 66
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 232831
Seq. ID LIB3272-002-P1-K1-H5
Method BLASTX
NCBI GI g3643609
BLAST score 431
E value 1.0e-42
Match length 134
% identity 64
NCBI Description (AC005395) putative Cys3His zinc finger protein
[Arabidopsis thaliana]

Seq. No. 232832
Seq. ID LIB3272-002-P1-K1-H7
Method BLASTX
NCBI GI g3834312
BLAST score 529
E value 4.0e-54
Match length 129
% identity 72
NCBI Description (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
Daucus carota and a member of S locus glycoprotein family
PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815,
gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248,
gb_AA728536, gb_Z30816 an

Seq. No. 232833
Seq. ID LIB3272-002-P1-K1-H8
Method BLASTX
NCBI GI g3915095
BLAST score 510
E value 7.0e-52
Match length 118
% identity 85
NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
>gi_1526537 dbj_BAA13414_ (D87520) cytochrome P450
(CYP73A14) [Glycyrrhiza echinata]

Seq. No. 232834
Seq. ID LIB3272-003-P1-K1-A1
Method BLASTX

090904-101000

```
Seq. No.      232841
Seq. ID      LIB3272-003-P1-K1-B12
Method       BLASTX
NCBI GI      g3176684
BLAST score   380
E value      1.0e-36
Match length  131
% identity    57
NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside
transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317,
gb_T20785, gb_AA586285 and gb_AA712578 come from this gene.
[Arabidopsis thaliana]
```

Seq. No.	232843
Seq. ID	LIB3272-003-P1-K1-B4
Method	BLASTX
NCBI GI	g3927825
BLAST score	513
E value	3.0e-52
Match length	100
% identity	95
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase

E value 1.0e-51
 Match length 93
 % identity 100
 NCBI Description ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No. 232850
 Seq. ID LIB3272-003-P1-K1-C5
 Method BLASTX
 NCBI GI g4263517
 BLAST score 407
 E value 8.0e-40
 Match length 128
 % identity 64
 NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]

Seq. No. 232851
 Seq. ID LIB3272-003-P1-K1-C6
 Method BLASTX
 NCBI GI g729668
 BLAST score 329
 E value 1.0e-30
 Match length 76
 % identity 86
 NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 232852
 Seq. ID LIB3272-003-P1-K1-C9
 Method BLASTX
 NCBI GI g1129145
 BLAST score 591
 E value 2.0e-61
 Match length 129
 % identity 87
 NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No. 232853
 Seq. ID LIB3272-003-P1-K1-D1
 Method BLASTX
 NCBI GI g1928981
 BLAST score 549
 E value 2.0e-56
 Match length 114
 % identity 95
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 232854
 Seq. ID LIB3272-003-P1-K1-D10


```
BLAST score      500
E value         1.0e-50
Match length    119
% identity      79
NCBI Description (AF092547) profilin [Ricinus communis]
```

```
Seq. No.      232870
Seq. ID       LIB3272-003-P1-K1-F3
Method        BLASTX
NCBI GI       g1709498
BLAST score    383
E value        1.0e-44
Match length   123
% identity     71
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
                thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                [Arabidopsis thaliana]
```

```
Seq. No.      232871
Seq. ID      LIB3272-003-P1-K1-F4
Method       BLASTX
NCBI GI      g3600030
BLAST score   299
E value      4.0e-27
Match length  106
% identity   54
NCBI Description (AF080119) contains similarity to ankyrin repeats (Pfam:
ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis
thaliana]
```

```
Seq. No.      232872
Seq. ID       LIB3272-003-P1-K1-F6
Method        BLASTX
NCBI GI       g112925
BLAST score    169
E value       7.0e-12
Match length   108
% identity     40
NCBI Description 41-2 PROTEIN ANTIGEN PRECURSOR >gi_320938_pir_A45503 41-2
protein antigen precursor - Plasmodium falciparum
>gi_160039 (J04656) 41-2 protein antigen [Plasmodium
falciparum]
```

```
Seq. No.      232873
Seq. ID      LIB3272-003-P1-K1-F7
Method       BLASTX
NCBI GI      g2760084
BLAST score   223
E value      2.0e-24
Match length  92
% identity   21
NCBI Description (Y16045) leucine-rich repeat protein [Arabidopsis thaliana]
```

Seq. No.	232874
Seq. ID	LIB3272-003-P1-K1-F8
Method	BLASTX

0366036-20000000

```
Seq. No.      232893
Seq. ID      LIB3272-004-P1-K1-A8
Method       BLASTX
NCBI GI      g2493144
BLAST score   224
E value      1.0e-18
Match length  66
% identity    73
NCBI Description  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir_S60132
H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
(clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585)
vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
thaliana]
```



```
Seq. No.      232894
Seq. ID      LIB3272-004-P1-K1-A9
Method       BLASTX
NCBI GI      g3377797
BLAST score   468
E value      6.0e-47
Match length  127
% identity    72
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for
by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
H36046; coded for by A. thaliana cDNA T44067; coded for by
A. thaliana cDNA T14056; coded for by A. thaliana cDNA
R90691 [Ara
```

Seq. No.	232895
Seq. ID	LIB3272-004-P1-K1-B1
Method	BLASTX
NCBI GI	g4235430
BLAST score	224
E value	9.0e-34
Match length	108
% identity	75
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]

```

Seq. No.      232896
Seq. ID       LIB3272-004-P1-K1-B11
Method        BLASTX
NCBI GI       g129881
BLAST score    688
E value       9.0e-73
Match length   141
% identity     93
NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                  (PPI-PFK) >gi_482294_pir_A36094
                  pyrophosphate--fructose 6-phosphate 1-phosphotransferase
                  (EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
                  >gi_169538 (M55190) pyrophosphate-fructose 6-phosphate
                  1-phosphotransferase alpha-subunit [Solanum tuberosum]

```

Seq. No.	232897
Seq. ID	LIB3272-004-P1-K1-B12
Method	BLASTX
NCBI GI	g3158474
BLAST score	478
E value	4.0e-48
Match length	116
% identity	83
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]

```
Seq. No.      232898
Seq: ID       LIB3272-004-P1-K1-B2
Method        BLASTX
NCBI GI       g3747050
BLAST score   417
```


0604019 70000

Seq. No.	232905
Seq. ID	LIB3272-004-P1-K1-C11
Method	BLASTX
NCBI GI	g2341034
BLAST score	535
E value	8.0e-55
Match length	109
% identity	97
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

```
Seq. No.      232907
Seq. ID      LIB3272-004-P1-K1-C3
Method       BLASTX
NCBI GI      g1076316
BLAST score   260
E value      1.0e-22
Match length  69
% identity   59
NCBI Description drought-induced protein Di19 - Arabidopsis thaliana
               >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
               thaliana]
```

33579

Match length 123
 % identity 72
 NCBI Description (AF038815) expansin [*Prunus armeniaca*]

Seq. No. 232934
 Seq. ID LIB3272-004-P1-K1-G3
 Method BLASTX
 NCBI GI g2494625
 BLAST score 214
 E value 3.0e-17
 Match length 84
 % identity 50
 NCBI Description HYPOTHETICAL PROTEIN KIAA0107 >gi_285951_dbj_BAA03497_
 (D14663) KIAA0107 [*Homo sapiens*]

Seq. No. 232935
 Seq. ID LIB3272-004-P1-K1-G4
 Method BLASTX
 NCBI GI g1709498
 BLAST score 488
 E value 2.0e-49
 Match length 113
 % identity 80
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - *Arabidopsis thaliana*
 >gi_887390_emb_CAA61411_ (X89008) osmotin [*Arabidopsis thaliana*]

Seq. No. 232936
 Seq. ID LIB3272-004-P1-K1-G6
 Method BLASTX
 NCBI GI g3080398
 BLAST score 217
 E value 2.0e-17
 Match length 112
 % identity 41
 NCBI Description (AL022603) putative protein [*Arabidopsis thaliana*]

Seq. No. 232937
 Seq. ID LIB3272-004-P1-K1-G7
 Method BLASTX
 NCBI GI g285286
 BLAST score 415
 E value 9.0e-41
 Match length 138
 % identity 57
 NCBI Description flavonol 4'-sulfotransferase - *Flaveria chloraefolia*

Seq. No. 232938
 Seq. ID LIB3272-004-P1-K1-G8
 Method BLASTX
 NCBI GI g3334147
 BLAST score 547
 E value 3.0e-56
 Match length 129
 % identity 81
 NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I

090816-10000

```
Seq. No.      232940
Seq. ID      LIB3272-004-P1-K1-H1
Method       BLASTX
NCBI GI      g2245089
BLAST score   157
E value      2.0e-10
Match length 103
% identity    39
NCBI Description (Z97343) asparagine--tRNA ligase homolog [Arabidopsis
thaliana]
```

```
Seq. No.      232941
Seq. ID       LIB3272-004-P1-K1-H11
Method        BLASTX
NCBI GI       g2760347
BLAST score    529
E value       3.0e-54
Match length   108
% identity     17
NCBI Description (U84968) ubiquitin [Arabidopsis thaliana]
```

```
Seq. No.      232942
Seq. ID      LIB3272-004-P1-K1-H12
Method       BLASTX
NCBI GI      g577301
BLAST score   180
E value      3.0e-13
Match length  130
% identity    33
NCBI Description (D42044) The ha3523 gene product is related to S.cerevisiae
gene product located in chromosome III. [Homo sapiens]
```

```
Seq. No.      232943
Seq. ID      LIB3272-004-P1-K1-H3
Method       BLASTX
NCBI GI      g542200
BLAST score   448
E value      1.0e-44
Match length  137
% identity    66
NCBI Description  hypothetical protein - garden asparagus
                  >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus
                  officinalis]
```

33586


```
Seq. ID      LIB3272-005-P1-K1-F12
Method      BLASTX
NCBI GI      g1928981
BLAST score  585
E value      1.0e-60
Match length 125
% identity   63
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
oleracea var. botrytis]
```

```
Seq. No.      232984
Seq. ID      LIB3272-005-P1-K1-F3
Method       BLASTX
NCBI GI      g1173209
BLAST score   269
E value      8.0e-24
Match length  77
% identity    73
NCBI Description  40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
protein S16 protein - upland cotton
>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
[Gossypium hirsutum]
```

```
Seq. No.      232985
Seq. ID       LIB3272-005-P1-K1-F5
Method        BLASTX
NCBI GI       g3641312
BLAST score    597
E value       4.0e-62
Match length   131
% identity     85
NCBI Description (AF087412) AJH2 [Arabidopsis thaliana]
```

```
Seq. No.      232986
Seq. ID      LIB3272-005-P1-K1-F7
Method       BLASTX
NCBI GI      g401329
BLAST score   159
E value      1.0e-10
Match length  110
% identity    33
NCBI Description  VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT)
>gi_542836_pir_JN0907 H+-transporting ATPase (EC 3.6.1.35)
chain C, vacuolar - human >gi_37643_emb_CAA48903_ (X69151)
vacuolar proton-ATPase [Homo sapiens]
>gi_4502315_ref_NP_001686.1_pATP6D_ATPase, H+
transporting, lysosomal (vacuolar proton pump) 42kD
```

```
Seq. No.      232987
Seq. ID      LIB3272-005-P1-K1-F8
Method       BLASTX
NCBI GI      g3510254
BLAST score   596
E value      6.0e-62
Match length  138
% identity    86
NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]
```


Match length <138
 % identity 90
 NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
 (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
 >gi_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No. 233004
 Seq. ID LIB3272-005-P1-K1-H9
 Method BLASTX
 NCBI GI g82308
 BLAST score 677
 E value 2.0e-71
 Match length 130
 % identity 91
 NCBI Description myb protein 308 - garden snapdragon

Seq. No. 233005
 Seq. ID LIB3272-006-P1-K1-A2
 Method BLASTX
 NCBI GI g2146746
 BLAST score 253
 E value 7.0e-22
 Match length 90
 % identity 58
 NCBI Description protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
 >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No. 233006
 Seq. ID LIB3272-006-P1-K1-A6
 Method BLASTX
 NCBI GI g70644
 BLAST score 515
 E value 1.0e-52
 Match length 111
 % identity 18
 NCBI Description ubiquitin precursor - common sunflower (fragment)

Seq. No. 233007
 Seq. ID LIB3272-006-P1-K1-A7
 Method BLASTX
 NCBI GI g2894607
 BLAST score 258
 E value 2.0e-22
 Match length 54
 % identity 87
 NCBI Description (AL021889) NAM (no apical meristem) - like protein
 [Arabidopsis thaliana]

Seq. No. 233008
 Seq. ID LIB3272-006-P1-K1-A8
 Method BLASTX
 NCBI GI g1170747
 BLAST score 206
 E value 2.0e-16
 Match length 43
 % identity 98
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345

(M88324) late embryogenesis-abundant protein [Gossypium
hirsutum] >gi_167347 (M37697) Lea5-A late
embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 233009
Seq. ID LIB3272-006-P1-K1-B10
Method BLASTX
NCBI GI g3128228
BLAST score 550
E value 1.0e-56
Match length 117
% identity 89
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis
thaliana] >gi_3337376 (AC004481) putative ribosomal protein
L18A [Arabidopsis thaliana]

Seq. No. 233010
Seq. ID LIB3272-006-P1-K1-B3
Method BLASTX
NCBI GI g4455206
BLAST score 371
E value 1.0e-35
Match length 129
% identity 60
NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis
thaliana]

Seq. No. 233011
Seq. ID LIB3272-006-P1-K1-B9
Method BLASTX
NCBI GI g543711
BLAST score 500
E value 1.0e-50
Match length 112
% identity 90
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796 pir_S30927 14-3-3
protein homolog - rice >gi_303859 dbj_BAA03711_ (D16140)
brain specific protein [Oryza sativa]

Seq. No. 233012
Seq. ID LIB3272-006-P1-K1-C2
Method BLASTX
NCBI GI g508304
BLAST score 273
E value 4.0e-24
Match length 65
% identity 78
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233013
Seq. ID LIB3272-006-P1-K1-C3
Method BLASTX
NCBI GI g167367
BLAST score 606
E value 4.0e-63
Match length 132
% identity 89

Seq. ID LIB3272-006-P1-K1-D12
 Method BLASTX
 NCBI GI g114420
 BLAST score 634
 E value 2.0e-66
 Match length 132
 % identity 94
 NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
 >gi_100882_pir_S11491 H⁺-transporting ATP synthase (EC
 3.6.1.34) beta chain, mitochondrial - maize
 >gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
 [Zea mays] >gi_897618 (M36087) F-1-ATPase subunit 2 [Zea
 mays]

Seq. No. 233020
 Seq. ID LIB3272-006-P1-K1-D2
 Method BLASTX
 NCBI GI g1709498
 BLAST score 513
 E value 3.0e-52
 Match length 113
 % identity 81
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34. PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 233021
 Seq. ID LIB3272-006-P1-K1-D3
 Method BLASTX
 NCBI GI g3450842
 BLAST score 142
 E value 9.0e-09
 Match length 110
 % identity 30
 NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza
 sativa]

Seq. No. 233022
 Seq. ID LIB3272-006-P1-K1-D5
 Method BLASTX
 NCBI GI g3329368
 BLAST score 181
 E value 3.0e-21
 Match length 125
 % identity 42
 NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 233023
 Seq. ID LIB3272-006-P1-K1-D6
 Method BLASTX
 NCBI GI g1168728
 BLAST score 321
 E value 9.0e-30
 Match length 113
 % identity 52
 NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883)

E value 7.0e-43
 Match length 133
 % identity 64
 NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233039
 Seq. ID LIB3272-006-P1-K1-G1
 Method BLASTX
 NCBI GI g2191150
 BLAST score 211
 E value 2.0e-21
 Match length 88
 % identity 68
 NCBI Description (AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No. 233040
 Seq. ID LIB3272-006-P1-K1-G10
 Method BLASTX
 NCBI GI g322596
 BLAST score 376
 E value 3.0e-36
 Match length 79
 % identity 92
 NCBI Description serine/threonine protein kinase (EC 2.7.-.-) AK21 - Arabidopsis thaliana >gi_166600 (M93023) SNF1-related protein kinase [Arabidopsis thaliana]
 >gi_1742969_emb_CAA64384_ (X94757) ser/thr protein kinase [Arabidopsis thaliana]

Seq. No. 233041
 Seq. ID LIB3272-006-P1-K1-G11
 Method BLASTX
 NCBI GI g1332579
 BLAST score 514
 E value 2.0e-52
 Match length 118
 % identity 9
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 233042
 Seq. ID LIB3272-006-P1-K1-G2
 Method BLASTX
 NCBI GI g730456
 BLAST score 488
 E value 2.0e-49
 Match length 115
 % identity 75
 NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 233043
 Seq. ID LIB3272-006-P1-K1-G3
 Method BLASTX
 NCBI GI g2462762
 BLAST score 329
 E value 1.0e-30
 Match length 122

Method BLASTX
 NCBI GI g2764941
 BLAST score 222
 E value 3.0e-18
 Match length 72
 % identity 58
 NCBI Description (X98255) transcriptionally stimulated by gibberellins;
 expressed in meristematic region, and style [Arabidopsis
 thaliana]

Seq. No. 233055
 Seq. ID LIB3272-007-P1-K1-A1
 Method BLASTX
 NCBI GI g2160166
 BLAST score 123
 E value 1.0e-09
 Match length 66
 % identity 58
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233056
 Seq. ID LIB3272-007-P1-K1-A12
 Method BLASTX
 NCBI GI g3158376
 BLAST score 328
 E value 9.0e-31
 Match length 95
 % identity 68
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233057
 Seq. ID LIB3272-007-P1-K1-A2
 Method BLASTX
 NCBI GI g4510363
 BLAST score 249
 E value 3.0e-21
 Match length 58
 % identity 81
 NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
 thaliana]

Seq. No. 233058
 Seq. ID LIB3272-007-P1-K1-A4
 Method BLASTX
 NCBI GI g2494905
 BLAST score 153
 E value 4.0e-10
 Match length 85
 % identity 45
 NCBI Description MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi_2132107_pir_S67174
 hypothetical protein YOR272w - yeast (Saccharomyces
 cerevisiae) >gi_1279699_emb_CAA61778_ (X89633) hypothetical
 protein [Saccharomyces cerevisiae]
 >gi_1420610_emb_CAA99497_ (Z75180) ORF YOR272w
 [Saccharomyces cerevisiae] >gi_1928989 (U92821)
 microtubule-associated protein [Saccharomyces cerevisiae]


```

Seq. No.          233059
Seq. ID           LIB3272-007-P1-K1-A6
Method            BLASTX
NCBI GI           g464986
BLAST score       366
E value           3.0e-35
Match length      69
% identity        97
NCBI Description   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir_S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_(Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi_600391_emb_CAA51201_(X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]
                  >gi_4455355_emb_CAB36765.1_(AL035524) ubiquitin-protein
                  ligase UBC9 [Arabidopsis thaliana]

```

```
Seq. No.      233060
Seq. ID      LIB3272-007-P1-K1-A7
Method       BLASTX
NCBI GI      g4538993
BLAST score   521
E value      3.0e-53
Match length  127
% identity    75
NCBI Description (AL049481) putative host response protein [Arabidopsis thaliana]
```

```
Seq. No.          233061
Seq. ID          LIB3272-007-P1-K1-A9
Method          BLASTX
NCBI GI         g2499946
BLAST score      575
E value         2.0e-59
Match length     134
% identity       84
NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana
                  tabacum]
```

```
Seq. No.      233062
Seq. ID      LIB3272-007-P1-K1-B1
Method       BLASTX
NCBI GI      g927575
BLAST score   405
E value      1.0e-39
Match length  90
% identity    77
NCBI Description (U12926) alpha galactosidase [Glycine max]
```

Seq. No.	233063
Seq. ID	LIB3272-007-P1-K1-B10
Method	BLASTX

catalase [Cucurbita pepo]

Seq. No. 233083
 Seq. ID LIB3272-007-P1-K1-E2
 Method BLASTX
 NCBI GI g3915826
 BLAST score 411
 E value 2.0e-40
 Match length 92
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 233084
 Seq. ID LIB3272-007-P1-K1-E3
 Method BLASTX
 NCBI GI g126770
 BLAST score 480
 E value 1.0e-48
 Match length 93
 % identity 97
 NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate
 synthase. (EC 4.1.3.2) - upland cotton
 >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
 [Gossypium hirsutum]

Seq. No. 233085
 Seq. ID LIB3272-007-P1-K1-E8
 Method BLASTX
 NCBI GI g232029
 BLAST score 373
 E value 4.0e-36
 Match length 74
 % identity 99
 NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
 >gi_100154_pir__S21989 translation elongation factor eEF-1
 alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)
 elongation factor 1A [Daucus carota]

Seq. No. 233086
 Seq. ID LIB3272-007-P1-K1-E9
 Method BLASTX
 NCBI GI g4204265
 BLAST score 396
 E value 1.0e-38
 Match length 93
 % identity 77
 NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 233087
 Seq. ID LIB3272-007-P1-K1-F1
 Method BLASTX
 NCBI GI g549063
 BLAST score 394
 E value 2.0e-38
 Match length 92
 % identity 82
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

Seq. ID	LIB3272-008-P1-K1-A3
Method	BLASTX
NCBI GI	g2149127
BLAST score	300
E value	2.0e-27
Match length	108
% identity	56
NCBI Description	(U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]
Seq. No.	233104
Seq. ID	LIB3272-008-P1-K1-A4
Method	BLASTX
NCBI GI	g3337356
BLAST score	566
E value	2.0e-58
Match length	118
% identity	93
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]
Seq. No.	233105
Seq. ID	LIB3272-008-P1-K1-A7
Method	BLASTX
NCBI GI	g2245136
BLAST score	446
E value	2.0e-44
Match length	120
% identity	68
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]
Seq. No.	233106
Seq. ID	LIB3272-008-P1-K1-A9
Method	BLASTX
NCBI GI	g3738301
BLAST score	395
E value	2.0e-38
Match length	104
% identity	64
NCBI Description	(AC005309) putative zinc-finger protein [Arabidopsis thaliana] >gi_4249397 (AC006072) putative zinc-finger protein (B-box zinc finger domain) [Arabidopsis thaliana]
Seq. No.	233107
Seq. ID	LIB3272-008-P1-K1-B10
Method	BLASTX
NCBI GI	g1001309
BLAST score	216
E value	2.0e-17
Match length	125
% identity	35
NCBI Description	(D64006) aspartate aminotransferase [Synechocystis sp.]
Seq. No.	233108
Seq. ID	LIB3272-008-P1-K1-B12
Method	BLASTX

Seq. No. 233113
 Seq. ID LIB3272-008-P1-K1-C11
 Method BLASTX
 NCBI GI g2244846
 BLAST score 463
 E value 2.0e-46
 Match length 118
 % identity 73
 NCBI Description (Z97337) ferredoxin [Arabidopsis thaliana]

Seq. No. 233114
 Seq. ID LIB3272-008-P1-K1-C12
 Method BLASTX
 NCBI GI g3395673
 BLAST score 450
 E value 7.0e-45
 Match length 116
 % identity 74
 NCBI Description (AB016623) RWC-3 [Oryza sativa]

Seq. No. 233115
 Seq. ID LIB3272-008-P1-K1-C2
 Method BLASTX
 NCBI GI g3024017
 BLAST score 509
 E value 9.0e-52
 Match length 99
 % identity 97
 NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No. 233116
 Seq. ID LIB3272-008-P1-K1-C4
 Method BLASTX
 NCBI GI g1518540
 BLAST score 512
 E value 4.0e-52
 Match length 108
 % identity 92
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 233117
 Seq. ID LIB3272-008-P1-K1-C5
 Method BLASTX
 NCBI GI g2129915
 BLAST score 186
 E value 4.0e-14
 Match length 72
 % identity 51
 NCBI Description ferredoxin precursor - sweet orange >gi_1360725_emb CAA87068_ (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No. 233118
 Seq. ID LIB3272-008-P1-K1-C8

Method BLASTX
 NCBI GI g3264769
 BLAST score 618
 E value 1.0e-64
 Match length 140
 % identity 57
 NCBI Description (AF071894) late embryogenesis-like protein [Prunus armeniaca]

Seq. No. 233119
 Seq. ID LIB3272-008-P1-K1-C9
 Method BLASTX
 NCBI GI g2132474
 BLAST score 177
 E value 7.0e-13
 Match length 63
 % identity 52
 NCBI Description probable membrane protein YDR091c - yeast (Saccharomyces cerevisiae) >gi_914875_emb_CAA90450_ (Z50111) unknown [Saccharomyces cerevisiae]

Seq. No. 233120
 Seq. ID LIB3272-008-P1-K1-D1
 Method BLASTX
 NCBI GI g3122785
 BLAST score 503
 E value 5.0e-51
 Match length 125
 % identity 82
 NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No. 233121
 Seq. ID LIB3272-008-P1-K1-D10
 Method BLASTX
 NCBI GI g441457
 BLAST score 648
 E value 4.0e-68
 Match length 122
 % identity 98
 NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No. 233122
 Seq. ID LIB3272-008-P1-K1-D3
 Method BLASTX
 NCBI GI g4193388
 BLAST score 253
 E value 8.0e-22
 Match length 76
 % identity 67
 NCBI Description (AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No. 233123
 Seq. ID LIB3272-008-P1-K1-D4
 Method BLASTX

NCBI GI g4336436
 BLAST score 493
 E value 6.0e-50
 Match length 139
 % identity 71
 NCBI Description (AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No. 233124
 Seq. ID LIB3272-008-P1-K1-D6
 Method BLASTX
 NCBI GI g2146797
 BLAST score 549
 E value 2.0e-56
 Match length 141
 % identity 74
 NCBI Description protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
 >gi_1134968 (U41385) protein disulphide isomerase PDI
 [Ricinus communis] >gi_1587210_prf_2206331A protein
 disulfide isomerase [Ricinus communis]

Seq. No. 233125
 Seq. ID LIB3272-008-P1-K1-D7
 Method BLASTX
 NCBI GI g508304
 BLAST score 218
 E value 1.0e-17
 Match length 76
 % identity 58
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233126
 Seq. ID LIB3272-008-P1-K1-E1
 Method BLASTX
 NCBI GI g3894171
 BLAST score 496
 E value 3.0e-50
 Match length 131
 % identity 69
 NCBI Description (AC005312) putative glutathione s-transferase [Arabidopsis
 thaliana]

Seq. No. 233127
 Seq. ID LIB3272-008-P1-K1-E10
 Method BLASTX
 NCBI GI g2435604
 BLAST score 172
 E value 9.0e-27
 Match length 139
 % identity 52
 NCBI Description (AF026213) strong similarity to Saccharomyces cerevisiae
 endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]

Seq. No. 233128
 Seq. ID LIB3272-008-P1-K1-E12
 Method BLASTX
 NCBI GI g2895870
 BLAST score 336

% identity 79
 NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 233144
 Seq. ID LIB3272-008-P1-K1-H11
 Method BLASTX
 NCBI GI g730463
 BLAST score 322
 E value 8.0e-30
 Match length 105
 % identity 59
 NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
 >gi_630323_pir_S44069 ribosomal protein L35a.e.c15 - yeast
 (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
 protein L37 [Saccharomyces cerevisiae]
 >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
 [Saccharomyces cerevisiae]

Seq. No. 233145
 Seq. ID LIB3272-008-P1-K1-H12
 Method BLASTX
 NCBI GI g2499946
 BLAST score 585
 E value 1.0e-60
 Match length 136
 % identity 85
 NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
 PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
 DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana
 tabacum]

Seq. No. 233146
 Seq. ID LIB3272-008-P1-K1-H2
 Method BLASTX
 NCBI GI g729470
 BLAST score 666
 E value 4.0e-70
 Match length 141
 % identity 90
 NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
 (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
 >gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2)
 precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
 (Z21493) mitochondrial formate dehydrogenase precursor
 [Solanum tuberosum]

Seq. No. 233147
 Seq. ID LIB3272-008-P1-K1-H3
 Method BLASTX
 NCBI GI g1170747
 BLAST score 353
 E value 2.0e-33
 Match length 84
 % identity 82
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
 (M88324) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167347 (M37697) Lea5-A late


```

BLAST score      261
E value          3.0e-46
Match length     120
% identity       76
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No.        233164
Seq. ID         LIB3272-009-P1-K1-C11
Method          BLASTX
NCBI GI         g4468979
BLAST score     304
E value         7.0e-28
Match length    68
% identity      84
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

```

```
Seq. No.      233165
Seq. ID      LIB3272-009-P1-K1-C2
Method       BLASTX
NCBI GI      g2791834
BLAST score   411
E value      1.0e-46
Match length  109
% identity    82
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
```

```
Seq. No.      233166
Seq. ID       LIB3272-009-P1-K1-C6
Method        BLASTX
NCBI GI       g1304227
BLAST score   532
E value       2.0e-54
Match length  133
% identity    73
NCBI Description (D63781) Epoxide hydrolase [Glycine max]
               >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase
               [Glycine max]
```

```
Seq. No.      233167
Seq. ID      LIB3272-009-P1-K1-C7
Method       BLASTX
NCBI GI      g67529
BLAST score   223
E value      3.0e-18
Match length  124
% identity    44
NCBI Description  membrane alanyl aminopeptidase (EC 3.4.11.2) - Escherichia coli
```

Seq. No.	233168
Seq. ID	LIB3272-009-P1-K1-C8
Method	BLASTX
NCBI GI	g529353
BLAST score	283
E value	3.0e-25
Match length	97
% identity	55


```
Seq. No.      233179
Seq. ID      LIB3272-009-P1-K1-E11
Method       BLASTX
NCBI GI      g2160166
BLAST score   460
E value      5.0e-46
Match length  133
% identity    64
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
```

```
Seq. No.      233180
Seq. ID      LIB3272-009-P1-K1-E12
Method       BLASTX
NCBI GI      g2500399
BLAST score   503
E value      4.0e-51
Match length  114
% identity    91
NCBI Description  40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098)
               ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls,
               embryos, Peptide, 253 aa] [Ambystoma mexicanum]
```

```
Seq. No.      233181
Seq. ID      LIB3272-009-P1-K1-E5
Method       BLASTX
NCBI GI      g1657621
BLAST score   395
E value      2.0e-38
Match length  117
% identity    67
NCBI Description (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
putative acyl-coA dehydrogenase [Arabidopsis thaliana]
```

```
Seq. No.          233182
Seq. ID          LIB3272-009-P1-K1-E6
Method           BLASTX
NCBI GI          g2146774
BLAST score      342
E value          1.0e-45
Match length     115
% identity       80
NCBI Description  serine acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis
                  thaliana >gi_905391 (U30298) serine acetyltransferase
                  [Arabidopsis thaliana]
```

```
Seq. No.      233183
Seq. ID      LIB3272-009-P1-K1-E7
Method       BLASTX
NCBI GI      g1332579
BLAST score   550
E value      1.0e-56
Match length  112
% identity   10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
```

Seq. No. 233184

% identity	82
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]
Seq. No.	233232
Seq. ID	LIB3272-010-P1-K1-E7
Method	BLASTX
NCBI GI	g4193388
BLAST score	298
E value	3.0e-27
Match length	70
% identity	81
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]
Seq. No.	233233
Seq. ID	LIB3272-010-P1-K1-E8
Method	BLASTX
NCBI GI	g3641868
BLAST score	197
E value	3.0e-15
Match length	50
% identity	76
NCBI Description	(AJ011012) hypothetical protein [Cicer arietinum]
Seq. No.	233234
Seq. ID	LIB3272-010-P1-K1-E9
Method	BLASTX
NCBI GI	g4218121
BLAST score	167
E value	1.0e-11
Match length	39
% identity	74
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]
Seq. No.	233235
Seq. ID	LIB3272-010-P1-K1-F1
Method	BLASTX
NCBI GI	g730449
BLAST score	484
E value	7.0e-49
Match length	113
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A) >gi_480647_pir_S37132 ribosomal protein L13.A - rape >gi_398918_emb_CAA80341_(Z22618) cold induced protein (BnC24A) [Brassica napus]
Seq. No.	233236
Seq. ID	LIB3272-010-P1-K1-F10
Method	BLASTX
NCBI GI	g1172977
BLAST score	427
E value	3.0e-42
Match length	100
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic

% identity 82
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
 (M88324) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167347 (M37697) Lea5-A late
 embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 233242
 Seq. ID LIB3272-010-P1-K1-F8
 Method BLASTX
 NCBI GI g3868758
 BLAST score 230
 E value 4.0e-19
 Match length 100
 % identity 63
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 233243
 Seq. ID LIB3272-010-P1-K1-F9
 Method BLASTX
 NCBI GI g3668089
 BLAST score 212
 E value 5.0e-17
 Match length 78
 % identity 47
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 233244
 Seq. ID LIB3272-010-P1-K1-G1
 Method BLASTX
 NCBI GI g1107526
 BLAST score 511
 E value 5.0e-52
 Match length 128
 % identity 75
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 233245
 Seq. ID LIB3272-010-P1-K1-G12
 Method BLASTX
 NCBI GI g431144
 BLAST score 201
 E value 9.0e-16
 Match length 116
 % identity 47
 NCBI Description (D21824) HSP70 [Lilium longiflorum]

Seq. No. 233246
 Seq. ID LIB3272-010-P1-K1-G7
 Method BLASTX
 NCBI GI g462195
 BLAST score 385
 E value 3.0e-37
 Match length 81
 % identity 91
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]


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% identity      80
NCBI Description (L22305) corC [Medicago sativa]

Seq. No.       233252
Seq. ID        LIB3272-011-P1-K1-A12
Method         BLASTX
NCBI GI        g2662343
BLAST score     606
E value        4.0e-63
Match length    116
% identity     100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No.       233253
Seq. ID        LIB3272-011-P1-K1-A3
Method         BLASTX
NCBI GI        g2662343
BLAST score     653
E value        1.0e-68
Match length    125
% identity     100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No.       233254
Seq. ID        LIB3272-011-P1-K1-A5
Method         BLASTX
NCBI GI        g1279588
BLAST score     405
E value        1.0e-39
Match length    114
% identity     68
NCBI Description (Z71749) glutathione S-transferase [Nicotiana
plumbaginifolia]

Seq. No.       233255
Seq. ID        LIB3272-011-P1-K1-A6
Method         BLASTX
NCBI GI        g1263291
BLAST score     565
E value        2.0e-58
Match length    117
% identity     88
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.       233256
Seq. ID        LIB3272-011-P1-K1-A8
Method         BLASTX
NCBI GI        g120669
BLAST score     229
E value        3.0e-19
Match length    54
% identity     81
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

```



```
Seq. No.      233257
Seq. ID      LIB3272-011-P1-K1-B1
Method       BLASTX
NCBI GI      g1170747
BLAST score   338
E value      1.0e-31
Match length  79
% identity    84
NCBI Description  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
(M88324) late embryogenesis-abundant protein [Gossypium
hirsutum] >gi_167347 (M37697) LeA5-A late
embryogenesis-abundant protein [Gossypium hirsutum]
```

```
Seq. No.      233258
Seq. ID      LIB3272-011-P1-K1-B11
Method       BLASTX
NCBI GI      g3033391
BLAST score   538
E value      3.0e-55
Match length  132
% identity    78
NCBI Description (AC004238) putative amino acid transporter [Arabidopsis thaliana]
```

```
Seq. No.      233259
Seq. ID       LIB3272-011-P1-K1-B2
Method        BLASTX
NCBI GI       g3953463
BLAST score   254
E value       7.0e-22
Match length  93
% identity    52
NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]
```

```
Seq. No.      233260
Seq. ID      LIB3272-011-P1-K1-B3
Method       BLASTX
NCBI GI      g3914605
BLAST score   348
E value      7.0e-33
Match length 117
% identity    61
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
                PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir_S39551
                ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                apple tree >gi_415852_emb_CAA79857_ (Z21794)
                ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                [Malus domestica]
```

Seq. No.	233261
Seq. ID	LIB3272-011-P1-K1-B8
Method	BLASTX
NCBI GI	g1632822
BLAST score	184
E value	6.0e-14
Match length	69

% identity 61
 NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
 (U77297) transmembrane protein [Oryza sativa]

Seq. No. 233262
 Seq. ID LIB3272-011-P1-K1-B9
 Method BLASTX
 NCBI GI g2160166
 BLAST score 328
 E value 1.0e-30
 Match length 130
 % identity 57
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233263
 Seq. ID LIB3272-011-P1-K1-C1
 Method BLASTX
 NCBI GI g1928981
 BLAST score 261
 E value 3.0e-23
 Match length 55
 % identity 93
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
 oleracea var. botrytis]

Seq. No. 233264
 Seq. ID LIB3272-011-P1-K1-C11
 Method BLASTX
 NCBI GI g2642154
 BLAST score 204
 E value 5.0e-16
 Match length 124
 % identity 44
 NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]
 >gi_3790595 (AF079186) RING-H2 finger protein RHC2a
 [Arabidopsis thaliana]

Seq. No. 233265
 Seq. ID LIB3272-011-P1-K1-C12
 Method BLASTX
 NCBI GI g3094012
 BLAST score 367
 E value 4.0e-35
 Match length 75
 % identity 87
 NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No. 233266
 Seq. ID LIB3272-011-P1-K1-C3
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 1.0e-14
 Match length 47
 % identity 68
 NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea
 batatas]

Seq. No. 233267
 Seq. ID LIB3272-011-P1-K1-C4
 Method BLASTX
 NCBI GI g3790569
 BLAST score 171
 E value 4.0e-12
 Match length 51
 % identity 53
 NCBI Description (AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana]

Seq. No. 233268
 Seq. ID LIB3272-011-P1-K1-C6
 Method BLASTX
 NCBI GI g2961372
 BLAST score 647
 E value 6.0e-68
 Match length 126
 % identity 94
 NCBI Description (AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 233269
 Seq. ID LIB3272-011-P1-K1-D1
 Method BLASTX
 NCBI GI g2583134
 BLAST score 198
 E value 2.0e-15
 Match length 62
 % identity 65
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No. 233270
 Seq. ID LIB3272-011-P1-K1-D11
 Method BLASTX
 NCBI GI g3643609
 BLAST score 434
 E value 5.0e-43
 Match length 134
 % identity 65
 NCBI Description (AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No. 233271
 Seq. ID LIB3272-011-P1-K1-D12
 Method BLASTX
 NCBI GI g4426565
 BLAST score 165
 E value 2.0e-11
 Match length 87
 % identity 40
 NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 233272

% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir_R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]
Seq. No.	233287
Seq. ID	LIB3272-011-P1-K1-G1
Method	BLASTX
NCBI GI	g231587
BLAST score	331
E value	4.0e-31
Match length	80
% identity	85
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_283001_pir_S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase [Oryza sativa]
Seq. No.	233288
Seq. ID	LIB3272-011-P1-K1-G10
Method	BLASTX
NCBI GI	g3643609
BLAST score	434
E value	5.0e-43
Match length	133
% identity	65
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]
Seq. No.	233289
Seq. ID	LIB3272-011-P1-K1-G11
Method	BLASTX
NCBI GI	g3334261
BLAST score	141
E value	1.0e-08
Match length	48
% identity	56
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1655851 (U61973) metallothionein-like protein [Malus domestica]
Seq. No.	233290
Seq. ID	LIB3272-011-P1-K1-G12
Method	BLASTX
NCBI GI	g629597
BLAST score	362
E value	1.0e-34
Match length	83
% identity	80
NCBI Description	proline-rich protein - rape >gi_545029_bbs_142669 (S6811) proline-rich SAC51 [Brassica napus=oilseed rape, pods, Peptide, 147 aa] [Brassica napus]
Seq. No.	233291
Seq. ID	LIB3272-011-P1-K1-G5
Method	BLASTX

NCBI GI g122085
 BLAST score 493
 E value 6.0e-50
 Match length 115
 % identity 87
 NCBI Description HISTONE H3 >gi_81641_pir_S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir_S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir_S57626 histone H3 - maize >gi_20251_emb_CAA31969_(X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_(X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493_(M36658) histone H3 (H3C3) [Zea mays] >gi_168495_(M13378) histone H3 [Zea mays] >gi_168497_(M13379) histone H3 [Zea mays] >gi_168506_(M35388) histone H3 [Zea mays] >gi_169655_(M77493) histone H3 [Petroselinum crispum] >gi_169657_(M77494) histone H3 [Petroselinum crispum] >gi_169659_(M77495) histone H3 [Petroselinum crispum] >gi_387565_(M17130) histone H3 [Arabidopsis thaliana] >gi_387567_(M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_(X84377) histone 3 [Zea mays] >gi_1040764_(M35387) histone H3 [Arabidopsis thaliana] >gi_1314779_(U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_(X82414) Histone H3 [Asparagus officinalis] >gi_1667592_(U77296) histone 3. [Oryza sativa] >gi_3249101_(AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf_1303352A histone H3 [Helicoverpa zea] >gi_225839_prf_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 233292
 Seq. ID LIB3272-011-P1-K1-H1
 Method BLASTX
 NCBI GI g120669
 BLAST score 576
 E value 1.0e-59
 Match length 114
 % identity 95
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_(X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 233293
 Seq. ID LIB3272-011-P1-K1-H2
 Method BLASTX
 NCBI GI g3759184
 BLAST score 283
 E value 3.0e-25
 Match length 135
 % identity 50
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 233294
 Seq. ID LIB3272-011-P1-K1-H3
 Method BLASTX

NCBI GI g2347098
 BLAST score 340
 E value 6.0e-32
 Match length 69
 % identity 90
 NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
 >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
 protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 233295
 Seq. ID LIB3272-011-P1-K1-H6
 Method BLASTX
 NCBI GI g3894178
 BLAST score 269
 E value 1.0e-23
 Match length 57
 % identity 86
 NCBI Description (AC005312) putative nucleic acid binding protein
 [Arabidopsis thaliana]

Seq. No. 233296
 Seq. ID LIB3272-011-P1-K1-H7
 Method BLASTX
 NCBI GI g1170748
 BLAST score 337
 E value 1.0e-31
 Match length 79
 % identity 84
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-D >gi_167349
 (M88323) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167351 (L01102) late embryogenesis-abundant
 protein [Gossypium hirsutum]

Seq. No. 233297
 Seq. ID LIB3272-012-P1-K1-A10
 Method BLASTX
 NCBI GI g508304
 BLAST score 261
 E value 9.0e-23
 Match length 61
 % identity 80
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233298
 Seq. ID LIB3272-012-P1-K1-A11
 Method BLASTX
 NCBI GI g4510373
 BLAST score 291
 E value 3.0e-26
 Match length 109
 % identity 56
 NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis
 thaliana]

Seq. No. 233299
 Seq. ID LIB3272-012-P1-K1-A12
 Method BLASTX

Method	BLASTX
NCBI GI	g1769903
BLAST score	376
E value	3.0e-36
Match length	118
% identity	59
NCBI Description	(X95738) proline transporter 2 [Arabidopsis thaliana]
Seq. No.	233305
Seq. ID	LIB3272-012-P1-K1-C11
Method	BLASTX
NCBI GI	g1666234
BLAST score	276
E value	5.0e-32
Match length	87
% identity	79
NCBI Description	(U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]
Seq. No.	233306
Seq. ID	LIB3272-012-P1-K1-C3
Method	BLASTX
NCBI GI	g2388575
BLAST score	261
E value	1.0e-22
Match length	130
% identity	40
NCBI Description	(AC000098) YUP8H12.18 [Arabidopsis thaliana]
Seq. No.	233307
Seq. ID	LIB3272-012-P1-K1-C4
Method	BLASTX
NCBI GI	g4335763
BLAST score	251
E value	2.0e-21
Match length	90
% identity	50
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.	233308
Seq. ID	LIB3272-012-P1-K1-C6
Method	BLASTX
NCBI GI	g3941543
BLAST score	193
E value	1.0e-14
Match length	54
% identity	70
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1) [Arabidopsis thaliana]
Seq. No.	233309
Seq. ID	LIB3272-012-P1-K1-C7
Method	BLASTX
NCBI GI	g3290020
BLAST score	518
E value	8.0e-53

PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and
gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No. 233315
Seq. ID LIB3272-012-P1-K1-D6
Method BLASTX
NCBI GI g4056494
BLAST score 255
E value 5.0e-22
Match length 130
% identity 50
NCBI Description (AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No. 233316
Seq. ID LIB3272-012-P1-K1-D7
Method BLASTX
NCBI GI g1483218
BLAST score 236
E value 9.0e-20
Match length 64
% identity 67
NCBI Description (X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No. 233317
Seq. ID LIB3272-012-P1-K1-D8
Method BLASTX
NCBI GI g2911060
BLAST score 291
E value 3.0e-26
Match length 113
% identity 38
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
>gi_3297826_emb_CAA19884.1_ (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 233318
Seq. ID LIB3272-012-P1-K1-D9
Method BLASTX
NCBI GI g1706918
BLAST score 250
E value 2.0e-21
Match length 107
% identity 49
NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277)
sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No. 233319
Seq. ID LIB3272-012-P1-K1-E12
Method BLASTX
NCBI GI g3955021
BLAST score 591
E value 2.0e-61
Match length 129
% identity 88
NCBI Description (AJ010811) HB2 homeodomain protein [Populus tremula x

090415-101000

```
Seq. No.      233321
Seq. ID      LIB3272-012-P1-K1-E7
Method       BLASTX
NCBI GI      g399392
BLAST score   323
E value      6.0e-30
Match length  107
% identity    65
NCBI Description  DIHYDROLIPOAMIDE DEHYDROGENASE PRECURSOR (GLYCINE CLEAVAGE
SYSTEM L PROTEIN) >gi_100037_pir_S22384 dihydrolipoamide
dehydrogenase (EC 1.8.1.4) - garden pea
>gi_20806_emb_CAA45066_(X63464) dihydrolipoamide
dehydrogenase [Pisum sativum]
```

```
Seq. No.      233322
Seq. ID      LIB3272-012-P1-K1-E8
Method       BLASTX
NCBI GI      g2267567
BLAST score   398
E value      9.0e-39
Match length  86
% identity    87
NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
protein 2 [Pelargonium x hortorum]
```

```
Seq. No.      233323
Seq. ID      LIB3272-012-P1-K1-F11
Method       BLASTX
NCBI GI      g3292817
BLAST score   249
E value      3.0e-21
Match length  80
% identity   68
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      233324
Seq. ID      LIB3272-012-P1-K1-F4
Method       BLASTX
NCBI GI      g2558655
BLAST score   157
E value      4.0e-18
Match length  77
% identity    64
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]
```



```
BLAST score      193
E value         8.0e-15
Match length    100
% identity      47
NCBI Description (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]
```

```
Seq. No.      233341
Seq. ID      LIB3272-013-P1-K1-A12
Method       BLASTX
NCBI GI      g2129759
BLAST score   493
E value      6.0e-50
Match length  128
% identity    78
NCBI Description  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
                >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate
                glucose epimerase [Arabidopsis thaliana]
```

```
Seq. No.      233342
Seq. ID      LIB3272-013-P1-K1-A2
Method       BLASTX
NCBI GI      g3204106
BLAST score   123
E value      9.0e-11
Match length  66
% identity   58
NCBI Description (AJ006763) putative beta-amylase [Cicer arietinum]
```

```
Seq. No.      233343
Seq. ID      LIB3272-013-P1-K1-A3
Method       BLASTX
NCBI GI      g2924509
BLAST score   274
E value      3.0e-24
Match length  95
% identity   55
NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis
thaliana]
```

```
Seq. No.      233344
Seq. ID      LIB3272-013-P1-K1-A6
Method       BLASTX
NCBI GI      g481236
BLAST score   246
E value      5.0e-21
Match length  60
% identity    80
NCBI Description  hypothetical protein - Madagascar periwinkle
                  >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
                  [Catharanthus roseus]
```

```
Seq. No.      233345
Seq. ID      LIB3272-013-P1-K1-A7
Method       BLASTX
NCBI GI      g2462753
BLAST score  172
```


E value 2.0e-12
 Match length 43
 % identity 72
 NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 233346
 Seq. ID LIB3272-013-P1-K1-A8
 Method BLASTX
 NCBI GI g3492806
 BLAST score 204
 E value 1.0e-17
 Match length 107
 % identity 55
 NCBI Description (AJ225045) adventitious rooting related oxygenase [Malus domestica]

Seq. No. 233347
 Seq. ID LIB3272-013-P1-K1-A9
 Method BLASTX
 NCBI GI g2462753
 BLAST score 168
 E value 7.0e-12
 Match length 43
 % identity 72
 NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 233348
 Seq. ID LIB3272-013-P1-K1-B1
 Method BLASTX
 NCBI GI g3252868
 BLAST score 224
 E value 2.0e-18
 Match length 77
 % identity 53
 NCBI Description (AF033536) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 233349
 Seq. ID LIB3272-013-P1-K1-B10
 Method BLASTX
 NCBI GI g4567301
 BLAST score 179
 E value 3.0e-13
 Match length 54
 % identity 63
 NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No. 233350
 Seq. ID LIB3272-013-P1-K1-B11
 Method BLASTX
 NCBI GI g1172873
 BLAST score 536
 E value 5.0e-55
 Match length 128
 % identity 70
 NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir_JN0719

drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - *Arabidopsis thaliana* >gi_435619_dbj_BAA02374_ (D13043) thiol protease [*Arabidopsis thaliana*]

```
Seq. No.      233351
Seq. ID      LIB3272_013-P1-K1-B12
Method       BLASTX
NCBI GI      g2213852
BLAST score   200
E value      1.0e-15
Match length  87
% identity    52
NCBI Description (AF003007) VVTL1 [Vitis vinifera]
```

```
Seq. No.      233352
Seq. ID      LIB3272-013-P1-K1-B3
Method       BLASTX
NCBI GI      g3868758
BLAST score   417
E value      5.0e-41
Match length  100
% identity    76
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
```

Seq. No.	233353
Seq. ID	LIB3272-013-P1-K1-B4
Method	BLASTX
NCBI GI	g2739365
BLAST score	540
E value	2.0e-55
Match length	119
% identity	80
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

```
Seq. No.      233354
Seq. ID       LIB3272-013-P1-K1-B6
Method        BLASTX
NCBI GI       g4006854
BLAST score    379
E value        1.0e-36
Match length   118
% identity     65
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      233355
Seq. ID       LIB3272-013-P1-K1-B9
Method        BLASTX
NCBI GI       g113621
BLAST score    483
E value        9.0e-49
Match length   108
% identity     88
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366 (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
```



```
Seq. No.      233361
Seq. ID      LIB3272-013-P1-K1-C8
Method       BLASTX
NCBI GI      g400650
BLAST score   183
E value      1.0e-13
Match length  93
% identity    42
NCBI Description  NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX
I-13KD-B) (CI-13KD-B) (B13) >gi_346535_pir_S28244 NADH
dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 -
bovine >gi_238_emb_CAA44903_ (X63218) NADH dehydrogenase
[Bos taurus]
```

```
Seq. No.      233362
Seq. ID      LIB3272-013-P1-K1-C9
Method       BLASTX
NCBI GI      g1658197
BLAST score   584
E value      1.0e-60
Match length  122
% identity    87
NCBI Description (U74630) calreticulin [Ricinus communis] >gi_1763297
                (U74631) calreticulin [Ricinus communis]
```

```
Seq. No.      233363
Seq. ID      LIB3272-013-P1-K1-D1
Method       BLASTX
NCBI GI      g3094012
BLAST score   360
E value      2.0e-34
Match length  75
% identity    85
NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
```

```
Seq. No.          233364
Seq. ID          LIB3272-013-P1-K1-D10
Method           BLASTX
NCBI GI          g2493130
BLAST score       625
E value          2.0e-65
Match length     121
% identity       100
NCBI Description  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B
                  SUBUNIT) >gi_459200 (U07053) vacuolar H+-ATPase subunit B
                  [Gossypium hirsutum]
```

```
Seq. No.      233365
Seq. ID      LIB3272-013-P1-K1-D11
Method       BLASTX
NCBI GI      g4323298
BLAST score   228
E value      7.0e-19
Match length  107
% identity    46
NCBI Description (AF099096) pulvinus outward-rectifying channel for
potassium SPOCK1 [Samanea saman]
```


Seq. No. 233366
 Seq. ID LIB3272-013-P1-K1-D4
 Method BLASTX
 NCBI GI g4567251
 BLAST score 514
 E value 2.0e-52
 Match length 123
 % identity 80
 NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 233367
 Seq. ID LIB3272-013-P1-K1-D6
 Method BLASTX
 NCBI GI g3080428
 BLAST score 321
 E value 9.0e-30
 Match length 98
 % identity 56
 NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 233368
 Seq. ID LIB3272-013-P1-K1-D7
 Method BLASTX
 NCBI GI g3851636
 BLAST score 474
 E value 9.0e-48
 Match length 108
 % identity 82
 NCBI Description (AF098519) unknown [Avicennia marina] >gi_4128206
 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 233369
 Seq. ID LIB3272-013-P1-K1-E1
 Method BLASTX
 NCBI GI g4510363
 BLAST score 348
 E value 6.0e-33
 Match length 81
 % identity 79
 NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No. 233370
 Seq. ID LIB3272-013-P1-K1-E10
 Method BLASTX
 NCBI GI g231536
 BLAST score 553
 E value 5.0e-57
 Match length 130
 % identity 81
 NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
 (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
 AMINOPEPTIDASE) >gi_99683_pir_S22399 leucyl aminopeptidase
 (EC 3.4.11.1) - Arabidopsis thaliana
 >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
 [Arabidopsis thaliana] >gi_4115380 (AC005967) putative

leucine aminopeptidase [Arabidopsis thaliana]

Seq. No. 233371
 Seq. ID LIB3272-013-P1-K1-E11
 Method BLASTX
 NCBI GI g2708484
 BLAST score 148
 E value 2.0e-09
 Match length 115
 % identity 38
 NCBI Description (U79557) IAA24 [Arabidopsis thaliana]

Seq. No. 233372
 Seq. ID LIB3272-013-P1-K1-E12
 Method BLASTX
 NCBI GI g122770
 BLAST score 341
 E value 2.0e-37
 Match length 112
 % identity 75
 NCBI Description HEMOGLOBIN II >gi_99509_pir_S13378 hemoglobin II - swamp
 oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina
 glauca]

Seq. No. 233373
 Seq. ID LIB3272-013-P1-K1-E2
 Method BLASTX
 NCBI GI g1166450
 BLAST score 321
 E value 9.0e-30
 Match length 71
 % identity 82
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

Seq. No. 233374
 Seq. ID LIB3272-013-P1-K1-E3
 Method BLASTX
 NCBI GI g2497538
 BLAST score 396
 E value 1.0e-38
 Match length 122
 % identity 71
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
 pyruvate kinase [Glycine max]

Seq. No. 233375
 Seq. ID LIB3272-013-P1-K1-E4
 Method BLASTX
 NCBI GI g416639
 BLAST score 154
 E value 3.0e-10
 Match length 76
 % identity 46
 NCBI Description INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG2
 >gi_287564_dbj_BAA03307_ (D14411) ORF [Vigna radiata]

Seq. No. 233376

NCBI Description (Z97336) CCAAT-binding transcription factor subunit
A(CBF-A) [Arabidopsis thaliana]

Seq. No. 233391
Seq. ID LIB3272-014-P1-K1-A1
Method BLASTX
NCBI GI g3334405
BLAST score 513
E value 2.0e-52
Match length 108
% identity 97
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
>gi_2267583 (AF009338) vacuolar H⁺-ATPase subunit E
[Gossypium hirsutum]

Seq. No. 233392
Seq. ID LIB3272-014-P1-K1-A10
Method BLASTX
NCBI GI g2347199
BLAST score 642
E value 2.0e-67
Match length 137
% identity 82
NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 233393
Seq. ID LIB3272-014-P1-K1-A11
Method BLASTX
NCBI GI g508304
BLAST score 241
E value 2.0e-20
Match length 82
% identity 57
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233394
Seq. ID LIB3272-014-P1-K1-A2
Method BLASTX
NCBI GI g3643594
BLAST score 458
E value 8.0e-46
Match length 125
% identity 74
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 233395
Seq. ID LIB3272-014-P1-K1-A4
Method BLASTX
NCBI GI g1709970
BLAST score 446
E value 2.0e-44
Match length 121
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 233396
Seq. ID LIB3272-014-P1-K1-A5

NCBI Description (AB007503) squalene synthase [Glycine max]

Seq. No. 233427
Seq. ID LIB3272-014-P1-K1-E5
Method BLASTX
NCBI GI g553107
BLAST score 399
E value 7.0e-39
Match length 114
% identity 68
NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]

Seq. No. 233428
Seq. ID LIB3272-014-P1-K1-E7
Method BLASTX
NCBI GI g2160166
BLAST score 304
E value 1.0e-27
Match length 128
% identity 55
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233429
Seq. ID LIB3272-014-P1-K1-E8
Method BLASTX
NCBI GI g4056494
BLAST score 306
E value 5.0e-28
Match length 100
% identity 61
NCBI Description (AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No. 233430
Seq. ID LIB3272-014-P1-K1-E9
Method BLASTX
NCBI GI g4467159
BLAST score 443
E value 5.0e-44
Match length 132
% identity 67
NCBI Description (AL035540) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233431
Seq. ID LIB3272-014-P1-K1-F1
Method BLASTX
NCBI GI g3334147
BLAST score 439
E value 1.0e-43
Match length 122
% identity 70
NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

Seq. No. 233432
Seq. ID LIB3272-014-P1-K1-F10
Method BLASTX

NCBI Description (AC006201) putative peptide methionine sulfoxide reductase [Arabidopsis thaliana]

Seq. No. 233438
 Seq. ID LIB3272-014-P1-K1-F9
 Method BLASTX
 NCBI GI g2500378
 BLAST score 434
 E value 5.0e-43
 Match length 95
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 233439
 Seq. ID LIB3272-014-P1-K1-G1
 Method BLASTX
 NCBI GI g1928981
 BLAST score 583
 E value 2.0e-60
 Match length 122
 % identity 63
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 233440
 Seq. ID LIB3272-014-P1-K1-G10
 Method BLASTX
 NCBI GI g3980415
 BLAST score 396
 E value 2.0e-38
 Match length 120
 % identity 62
 NCBI Description (AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No. 233441
 Seq. ID LIB3272-014-P1-K1-G2
 Method BLASTX
 NCBI GI g629483
 BLAST score 338
 E value 1.0e-31
 Match length 122
 % identity 56
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula pendula]

Seq. No. 233442
 Seq. ID LIB3272-014-P1-K1-G4
 Method BLASTX
 NCBI GI g2244847
 BLAST score 311
 E value 1.0e-28
 Match length 119
 % identity 55
 NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog

00684016-101000

Seq. No. 233448

Method BLASTX
 NCBI GI g2262173
 BLAST score 376
 E value 3.0e-36
 Match length 137
 % identity 57
 NCBI Description (AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No. 233459
 Seq. ID LIB3272-015-P1-K1-B6
 Method BLASTX
 NCBI GI g2961372
 BLAST score 355
 E value 9.0e-47
 Match length 114
 % identity 85
 NCBI Description (AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 233460
 Seq. ID LIB3272-015-P1-K1-B7
 Method BLASTX
 NCBI GI g267069
 BLAST score 382
 E value 4.0e-37
 Match length 72
 % identity 96
 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 233461
 Seq. ID LIB3272-015-P1-K1-B9
 Method BLASTX
 NCBI GI g1703108
 BLAST score 490
 E value 1.0e-49
 Match length 90
 % identity 100
 NCBI Description ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No. 233462
 Seq. ID LIB3272-015-P1-K1-C10
 Method BLASTX
 NCBI GI g3193298
 BLAST score 364
 E value 9.0e-35
 Match length 110
 % identity 63
 NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]

00684016-101000

Seq. No. 233463
Seq. ID LIB3272-015-P1-K1-C2
Method BLASTX
NCBI GI g3158376
BLAST score 165
E value 6.0e-21
Match length 106
% identity 55
NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233464
Seq. ID LIB3272-015-P1-K1-C6
Method BLASTX
NCBI GI g629483
BLAST score 334
E value 3.0e-31
Match length 122
% identity 55
NCBI Description gene 1-Sc3 protein - European white birch
>gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
>gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
pendula]

Seq. No. 233465
Seq. ID LIB3272-015-P1-K1-C7
Method BLASTX
NCBI GI g2231034
BLAST score 576
E value 1.0e-59
Match length 125
% identity 87
NCBI Description (Y12785) MAP kinase I [Petroselinum crispum]

Seq. No. 233466
Seq. ID LIB3272-015-P1-K1-C9
Method BLASTX
NCBI GI g3482918
BLAST score 589
E value 4.0e-61
Match length 130
% identity 89
NCBI Description (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
thaliana]

Seq. No. 233467
Seq. ID LIB3272-015-P1-K1-D1
Method BLASTX
NCBI GI g2129605
BLAST score 290
E value 2.0e-26
Match length 65
% identity 85
NCBI Description GTP-binding protein 2 - Arabidopsis thaliana
>gi_2129702_pir_S71585 Rab2 homolog GTP-binding protein
ATGB2 - Arabidopsis thaliana >gi_1184983 (U46925) ATGB2
[Arabidopsis thaliana] >gi_3805852_emb_CAA21472_ (AL031986)

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```
Seq. No.      233468
Seq. ID      LIB3272-015-P1-K1-D10
Method       BLASTX
NCBI GI      g1703375
BLAST score   610
E value      1.0e-63
Match length  120
% identity    99
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
               DcARF1 [Daucus carota]
```

Seq. No.	233469
Seq. ID	LIB3272-015-P1-K1-D12
Method	BLASTX
NCBI GI	g2911039
BLAST score	498
E value	2.0e-50
Match length	125
% identity	70
NCBI Description	(AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]

```
Seq. No.      233470
Seq. ID      LIB3272-015-P1-K1-D2
Method       BLASTX
NCBI GI      g2662343
BLAST score   546
E value      4.0e-56
Match length  105
% identity    99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
```

```
Seq. No.      233471
Seq. ID      LIB3272-015-P1-K1-D4
Method       BLASTX
NCBI GI      g2191150
BLAST score   286
E value      1.0e-25
Match length  90
% identity    69
NCBI Description (AF007269) similar to mitochondrial carrier family
               [Arabidopsis thaliana]
```

```
Seq. No.      233472
Seq. ID       LIB3272-015-P1-K1-D5
Method        BLASTX
NCBI GI       g1843527
BLAST score   694
E value       2.0e-73
Match length  137
% identity    56
NCBI Description (U73747) annexin [Gossypium hirsutum]
```

Seq. No.	233473
Seq. ID	LIB3272-015-P1-K1-D6

Method BLASTX
 NCBI GI g416649
 BLAST score 367
 E value 4.0e-35
 Match length 111
 % identity 63
 NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT1/PCNT110) >gi_100303_pir_S16267 auxin-induced protein (clone pGNT1) - common tobacco >gi_19789_emb_CAA39709_ (X56268) auxin-induced protein [Nicotiana tabacum] >gi_19795_emb_CAA39705_ (X56264) auxin-induced protein [Nicotiana tabacum]

Seq. No. 233474
 Seq. ID LIB3272-015-P1-K1-D9
 Method BLASTX
 NCBI GI g464986
 BLAST score 577
 E value 9.0e-60
 Match length 108
 % identity 99
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 233475
 Seq. ID LIB3272-015-P1-K1-E1
 Method BLASTX
 NCBI GI g2129889
 BLAST score 524
 E value 1.0e-53
 Match length 102
 % identity 97
 NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea

Seq. No. 233476
 Seq. ID LIB3272-015-P1-K1-E11
 Method BLASTX
 NCBI GI g2970654
 BLAST score 321
 E value 1.0e-29
 Match length 111
 % identity 66
 NCBI Description (AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No. 233477
 Seq. ID LIB3272-015-P1-K1-E4
 Method BLASTX

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 233488
 Seq. ID LIB3272-015-P1-K1-F8
 Method BLASTX
 NCBI GI g1709651
 BLAST score 421
 E value 2.0e-41
 Match length 132
 % identity 63
 NCBI Description PLASTOCYANIN A PRECURSOR >gi_2117431_pir_S58209
 plastocyanin a precursor - black poplar
 >gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus
 nigra]

Seq. No. 233489
 Seq. ID LIB3272-015-P1-K1-G3
 Method BLASTX
 NCBI GI g464986
 BLAST score 531
 E value 2.0e-54
 Match length 98
 % identity 99
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
 LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC
 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
 enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
 ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
 enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1 (AL035524) ubiquitin-protein
 ligase UBC9 [Arabidopsis thaliana]

Seq. No. 233490
 Seq. ID LIB3272-015-P1-K1-G4
 Method BLASTX
 NCBI GI g2462762
 BLAST score 354
 E value 1.0e-33
 Match length 128
 % identity 58
 NCBI Description (AC002292) Highly similar to auxin-induced protein
 (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 233491
 Seq. ID LIB3272-015-P1-K1-G7
 Method BLASTX
 NCBI GI g1173256
 BLAST score 616
 E value 3.0e-64
 Match length 140
 % identity 86
 NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal
 protein S4 - upland cotton >gi_488739_emb_CAA55882_
 (X79300) ribosomal protein, small subunit 4e (RS4e)


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NCBI GI      g267072
BLAST score   161
E value       3.0e-11
Match length  66
% identity    52
NCBI Description  TUBULIN BETA-1 CHAIN >gi_100072_pir_S20868 tubulin beta-1
chain - garden pea >gi_20758_emb_CAA38613_ (X54844)
beta-tubulin 1 [Pisum sativum]

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Seq. No.      233518
Seq. ID      LIB3272-016-P1-K1-C11
Method       BLASTX
NCBI GI      g629483
BLAST score   309
E value      2.0e-28
Match length 115
% identity   56
NCBI Description gene 1-Sc3 protein - European white birch
>gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
>gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
pendula]
```

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Seq. No.          233519
Seq. ID          LIB3272-016-P1-K1-C2
Method           BLASTX
NCBI GI          g266945
BLAST score      528
E value          5.0e-54
Match length     121
% identity       88
NCBI Description  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                  >gi_100065_pir_S19978 ribosomal protein L9 - garden pea
                  >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                  >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                  [Pisum sativum]
```

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Seq. No.          233520
Seq. ID           LIB3272-016-P1-K1-C5
Method            BLASTX
NCBI GI           g3023847
BLAST score       523
E value           2.0e-53
Match length      108
% identity        35
NCBI Description   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                  PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                  subunit-like [Medicago sativa]
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Seq. No.	233521
Seq. ID	LIB3272-016-P1-K1-C6
Method	BLASTX
NCBI GI	g2499946
BLAST score	526
E value	8.0e-54
Match length	128
% identity	80
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana
tabacum]

Seq. No. 233522
Seq. ID LIB3272-016-P1-K1-C7
Method BLASTX
NCBI GI g2209384
BLAST score 421
E value 2.0e-41
Match length 96
% identity 88
NCBI Description (AF008441) glutathione reductase [Brassica rapa]

Seq. No. 233523
Seq. ID LIB3272-016-P1-K1-D1
Method BLASTX
NCBI GI g1709498
BLAST score 490
E value 1.0e-49
Match length 107
% identity 82
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
>gi_1362001_pir_S57524.osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
[Arabidopsis thaliana]

Seq. No. 233524
Seq. ID LIB3272-016-P1-K1-D11
Method BLASTX
NCBI GI g464365
BLAST score 492
E value 8.0e-50
Match length 128
% identity 76
NCBI Description PEROXIDASE P7 >gi_66306_pir_OPNB7 peroxidase (EC 1.11.1.7)
- turnip

Seq. No. 233525
Seq. ID LIB3272-016-P1-K1-D4
Method BLASTX
NCBI GI g3885884
BLAST score 449
E value 1.0e-44
Match length 101
% identity 86
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 233526
Seq. ID LIB3272-016-P1-K1-D6
Method BLASTX
NCBI GI g1170747
BLAST score 285
E value 1.0e-25
Match length 70
% identity 81
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345

(M88324) late embryogenesis-abundant protein [Gossypium
hirsutum] >gi_167347 (M37697) Lea5-A late
embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 233527
Seq. ID LIB3272-016-P1-K1-E10
Method BLASTX
NCBI GI g3309243
BLAST score 609
E value 1.0e-63
Match length 127
% identity 91
NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus
limon]

Seq. No. 233528
Seq. ID LIB3272-016-P1-K1-E12
Method BLASTX
NCBI GI g1449179
BLAST score 591
E value 2.0e-61
Match length 127
% identity 93
NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein
[Nicotiana tabacum]

Seq. No. 233529
Seq. ID LIB3272-016-P1-K1-E2
Method BLASTX
NCBI GI g1170747
BLAST score 184
E value 2.0e-22
Match length 72
% identity 76
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
(M88324) late embryogenesis-abundant protein [Gossypium
hirsutum] >gi_167347 (M37697) Lea5-A late
embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 233530
Seq. ID LIB3272-016-P1-K1-E3
Method BLASTX
NCBI GI g4519264
BLAST score 630
E value 5.0e-66
Match length 128
% identity 98
NCBI Description (AB024277) vacuolar H⁺-ATPase B subunit [Citrus unshiu]

Seq. No. 233531
Seq. ID LIB3272-016-P1-K1-E4
Method BLASTX
NCBI GI g1848212
BLAST score 591
E value 2.0e-61
Match length 127
% identity 43

Match length 71
 % identity 58
 NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 233547
 Seq. ID LIB3272-016-P1-K1-H7
 Method BLASTX
 NCBI GI g1245182
 BLAST score 461
 E value 3.0e-46
 Match length 110
 % identity 77
 NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No. 233548
 Seq. ID LIB3272-017-P1-K1-A1
 Method BLASTX
 NCBI GI g4263776
 BLAST score 326
 E value 3.0e-30
 Match length 142
 % identity 55
 NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
 >gi_4510390_gb_AAD21478.1_ (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 233549
 Seq. ID LIB3272-017-P1-K1-A11
 Method BLASTX
 NCBI GI g462195
 BLAST score 434
 E value 5.0e-43
 Match length 90
 % identity 93
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
 >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 233550
 Seq. ID LIB3272-017-P1-K1-A5
 Method BLASTX
 NCBI GI g1717949
 BLAST score 314
 E value 6.0e-29
 Match length 74
 % identity 77
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1
 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1)
 >gi_100375_pir_B41607 ubiquinol--cytochrome-c reductase
 (EC 1.10.2.2) iron-sulfur protein precursor - common
 tobacco (fragment) >gi_170322 (M77225) Rieske Fe-S protein [Nicotiana tabacum]

Seq. No. 233551
 Seq. ID LIB3272-017-P1-K1-A9

% identity	50
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]
Seq. No.	233562
Seq. ID	LIB3272-017-P1-K1-C4
Method	BLASTX
NCBI GI	g441457
BLAST score	634
E value	2.0e-66
Match length	119
% identity	98
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]
Seq. No.	233563
Seq. ID	LIB3272-017-P1-K1-C5
Method	BLASTX
NCBI GI	g4105798
BLAST score	93
E value	5.0e-09
Match length	58
% identity	59
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.	233564
Seq. ID	LIB3272-017-P1-K1-C6
Method	BLASTX
NCBI GI	g3901014
BLAST score	235
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]
Seq. No.	233565
Seq. ID	LIB3272-017-P1-K1-C7
Method	BLASTX
NCBI GI	g2909783
BLAST score	413
E value	1.0e-40
Match length	138
% identity	63
NCBI Description	(AF020289) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]
Seq. No.	233566
Seq. ID	LIB3272-017-P1-K1-D1
Method	BLASTX
NCBI GI	g3747050
BLAST score	425
E value	6.0e-42
Match length	106
% identity	77
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]
Seq. No.	233567

Seq. ID LIB3272-017-P1-K1-D10
 Method BLASTX
 NCBI GI g1684857
 BLAST score 623
 E value 4.0e-65
 Match length 126
 % identity 40
 NCBI Description (U77940) polyubiquitin [Phaseolus vulgaris]

Seq. No. 233568
 Seq. ID LIB3272-017-P1-K1-D11
 Method BLASTX
 NCBI GI g3080440
 BLAST score 151
 E value 8.0e-10
 Match length 53
 % identity 58
 NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233569
 Seq. ID LIB3272-017-P1-K1-D12
 Method BLASTX
 NCBI GI g2160166
 BLAST score 332
 E value 5.0e-31
 Match length 131
 % identity 57
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233570
 Seq. ID LIB3272-017-P1-K1-D5
 Method BLASTX
 NCBI GI g267131
 BLAST score 186
 E value 7.0e-14
 Match length 86
 % identity 16
 NCBI Description NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN)
 >gi_423120_pir_A46174 RNA-binding protein TIAR - human
 >gi_189310 (M96954) nucleolysin TIAR [Homo sapiens]
 >gi_4507499_ref_NP_003243.1_pTIAL1_TIA1 cytotoxic
 granule-associated RNA-binding protein-like

Seq. No. 233571
 Seq. ID LIB3272-017-P1-K1-D6
 Method BLASTX
 NCBI GI g4056469
 BLAST score 581
 E value 3.0e-60
 Match length 113
 % identity 100
 NCBI Description (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
 factor from Arabidopsis thaliana. ESTs gb_Z25826,
 gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
 gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and
 gb_Z25043 come from t

NCBI GI g508304
 BLAST score 216
 E value 2.0e-17
 Match length 75
 % identity 59
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233613
 Seq. ID LIB3272-018-P1-K1-B12
 Method BLASTX
 NCBI GI g3901014
 BLAST score 235
 E value 1.0e-19
 Match length 55
 % identity 76
 NCBI Description (AJ130886) metallothionein-like protein class II [Fagus sylvatica]

Seq. No. 233614
 Seq. ID LIB3272-018-P1-K1-B2
 Method BLASTX
 NCBI GI g2507442
 BLAST score 166
 E value 4.0e-12
 Match length 42
 % identity 74
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1419685_emb_CAA67207_ (X98618) TCTP-like protein
 [Medicago sativa]

Seq. No. 233615
 Seq. ID LIB3272-018-P1-K1-B3
 Method BLASTX
 NCBI GI g1944403
 BLAST score 468
 E value 6.0e-47
 Match length 127
 % identity 73
 NCBI Description (D86590) cinnamyl alcohol dehydrogenase [Zinnia elegans]

Seq. No. 233616
 Seq. ID LIB3272-018-P1-K1-B4
 Method BLASTX
 NCBI GI g2695711
 BLAST score 526
 E value 1.0e-53
 Match length 118
 % identity 81
 NCBI Description (AJ001370) cytochrome b5 [Olea europaea]

Seq. No. 233617
 Seq. ID LIB3272-018-P1-K1-B5
 Method BLASTX
 NCBI GI g3176691
 BLAST score 395
 E value 2.0e-38
 Match length 121

% identity 36
 NCBI Description (AC003671) Contains homology to serine/threonine protein kinase gb_X99618 from Mycobacterium tuberculosis. ESTs gb_F14403, gb_F14404, and gb_N96730 come from this gene. [Arabidopsis thaliana]

Seq. No. 233618
 Seq. ID LIB3272-018-P1-K1-B7
 Method BLASTX
 NCBI GI g4262174
 BLAST score 236
 E value 2.0e-20
 Match length 50
 % identity 80
 NCBI Description (AC005508) 9058 [Arabidopsis thaliana]

Seq. No. 233619
 Seq. ID LIB3272-018-P1-K1-B8
 Method BLASTX
 NCBI GI g3694872
 BLAST score 384
 E value 2.0e-37
 Match length 80
 % identity 88
 NCBI Description (AF092547) profilin [Ricinus communis]

Seq. No. 233620
 Seq. ID LIB3272-018-P1-K1-B9
 Method BLASTX
 NCBI GI g2677828
 BLAST score 456
 E value 1.0e-45
 Match length 118
 % identity 70
 NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No. 233621
 Seq. ID LIB3272-018-P1-K1-C1
 Method BLASTX
 NCBI GI g2459417
 BLAST score 382
 E value 7.0e-37
 Match length 143
 % identity 56
 NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No. 233622
 Seq. ID LIB3272-018-P1-K1-C11
 Method BLASTX
 NCBI GI g1665867
 BLAST score 456
 E value 1.0e-45
 Match length 117
 % identity 70
 NCBI Description (Y09123) aspartic proteinase [Centaurea calcitrapa]

NCBI GI g1170247
 BLAST score 520
 E value 5.0e-53
 Match length 122
 % identity 71
 NCBI Description HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880)
 pre-hevein-like protein [Arabidopsis thaliana]

Seq. No. 233634
 Seq. ID LIB3272-018-P1-K1-D5
 Method BLASTX
 NCBI GI g1107526
 BLAST score 569
 E value 8.0e-59
 Match length 138
 % identity 80
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 233635
 Seq. ID LIB3272-018-P1-K1-D7
 Method BLASTX
 NCBI GI g2792297
 BLAST score 261
 E value 1.0e-22
 Match length 77
 % identity 58
 NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 233636
 Seq. ID LIB3272-018-P1-K1-D8
 Method BLASTX
 NCBI GI g3309243
 BLAST score 611
 E value 1.0e-63
 Match length 124
 % identity 94
 NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus
 limon]

Seq. No. 233637
 Seq. ID LIB3272-018-P1-K1-D9
 Method BLASTX
 NCBI GI g1657948
 BLAST score 283
 E value 2.0e-25
 Match length 56
 % identity 91
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 233638
 Seq. ID LIB3272-018-P1-K1-E11
 Method BLASTX
 NCBI GI g4185515
 BLAST score 239
 E value 2.0e-20
 Match length 78
 % identity 63

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NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]
Seq. No.	233639
Seq. ID	LIB3272-018-P1-K1-E12
Method	BLASTX
NCBI GI	g3892056
BLAST score	274
E value	2.0e-24
Match length	72
% identity	76
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
Seq. No.	233640
Seq. ID	LIB3272-018-P1-K1-E2
Method	BLASTX
NCBI GI	g1839188
BLAST score	459
E value	7.0e-46
Match length	102
% identity	84
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.	233641
Seq. ID	LIB3272-018-P1-K1-E3
Method	BLASTX
NCBI GI	g4539545
BLAST score	685
E value	2.0e-72
Match length	135
% identity	98
NCBI Description	(Y16644) PRC1 [Nicotiana tabacum]
Seq. No.	233642
Seq. ID	LIB3272-018-P1-K1-E4
Method	BLASTX
NCBI GI	g1699024
BLAST score	410
E value	3.0e-40
Match length	116
% identity	66
NCBI Description	(U78866) gene1000 [Arabidopsis thaliana] >gi_1699057 (U78870) unknown [Arabidopsis thaliana]
Seq. No.	233643
Seq. ID	LIB3272-018-P1-K1-E8
Method	BLASTX
NCBI GI	g3885328
BLAST score	208
E value	2.0e-16
Match length	126
% identity	33
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	233644
Seq. ID	LIB3272-018-P1-K1-E9

Method	BLASTX
NCBI GI	g2462758
BLAST score	377
E value	3.0e-36
Match length	126
% identity	60
NCBI Description	(AC002292) putative RNA-binding protein [Arabidopsis thaliana]
Seq. No.	233645
Seq. ID	LIB3272-018-P1-K1-F11
Method	BLASTX
NCBI GI	g3482967
BLAST score	250
E value	8.0e-22
Match length	58
% identity	81
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	233646
Seq. ID	LIB3272-018-P1-K1-F2
Method	BLASTX
NCBI GI	g1351411
BLAST score	502
E value	6.0e-51
Match length	122
% identity	75
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B) >gi_1076553_pir_S49175 cysteine proteinase precursor - spring vetch >gi_2129906_pir_S68984 cysteine proteinase precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899) cysteine proteinase [Vicia sativa]
Seq. No.	233647
Seq. ID	LIB3272-018-P1-K1-F4
Method	BLASTX
NCBI GI	g2191150
BLAST score	166
E value	1.0e-11
Match length	67
% identity	63
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]
Seq. No.	233648
Seq. ID	LIB3272-018-P1-K1-G5
Method	BLASTX
NCBI GI	g2462748
BLAST score	591
E value	2.0e-61
Match length	122
% identity	93
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

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thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No. 233654
 Seq. ID LIB3272-018-P1-K1-H6
 Method BLASTX
 NCBI GI g2078350
 BLAST score 159
 E value 8.0e-11
 Match length 77
 % identity 48
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 233655
 Seq. ID LIB3272-018-P1-K1-H8
 Method BLASTX
 NCBI GI g456568
 BLAST score 165
 E value 1.0e-11
 Match length 47
 % identity 66
 NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No. 233656
 Seq. ID LIB3272-018-P1-K1-H9
 Method BLASTX
 NCBI GI g4056469
 BLAST score 508
 E value 6.0e-68
 Match length 141
 % identity 97
 NCBI Description (AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No. 233657
 Seq. ID LIB3272-019-P1-K1-A1
 Method BLASTX
 NCBI GI g3641312
 BLAST score 545
 E value 5.0e-56
 Match length 121
 % identity 84
 NCBI Description (AF087412) AJH2 [Arabidopsis thaliana]

Seq. No. 233658
 Seq. ID LIB3272-019-P1-K1-A10
 Method BLASTX
 NCBI GI g3334147
 BLAST score 535
 E value 6.0e-55
 Match length 121
 % identity 83
 NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I chitinase [Gossypium hirsutum]

NCBI GI g2879867
 BLAST score 412
 E value 2.0e-40
 Match length 115
 % identity 68
 NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces pombe]

Seq. No. 233678
 Seq. ID LIB3272-019-P1-K1-D8
 Method BLASTX
 NCBI GI g1928981
 BLAST score 505
 E value 2.0e-51
 Match length 112
 % identity 90
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 233679
 Seq. ID LIB3272-019-P1-K1-D9
 Method BLASTX
 NCBI GI g3901018
 BLAST score 294
 E value 2.0e-26
 Match length 109
 % identity 56
 NCBI Description (AJ130889) stress and pathogenesis-related protein [Fagus sylvatica]

Seq. No. 233680
 Seq. ID LIB3272-019-P1-K1-E10
 Method BLASTX
 NCBI GI g2618721
 BLAST score 164
 E value 2.0e-11
 Match length 77
 % identity 55
 NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 233681
 Seq. ID LIB3272-019-P1-K1-E4
 Method BLASTX
 NCBI GI g2833386
 BLAST score 347
 E value 8.0e-33
 Match length 91
 % identity 79
 NCBI Description RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi_2129493_pir_S62724 ribulose-phosphate 3-epimerase (EC 5.1.1.3.1) precursor - spinach >gi_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi_3264788 (AF070941) ribulose-phosphate 3-epimerase [Spinacia oleracea] >gi_1587969_prf_2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. ID LIB3272-020-P1-K1-D9
Method BLASTX
NCBI GI g132944
BLAST score 612
E value 7.0e-64
Match length 121
% identity 92
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir_JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 233734
Seq. ID LIB3272-020-P1-K1-E11
Method BLASTX
NCBI GI g3789799
BLAST score 210
E value 9.0e-17
Match length 127
% identity 9
NCBI Description (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens] >gi_4557445_ref_NP_001259.1_pCHC1L RCC1-like G exchanging factor RLG

Seq. No. 233735
Seq. ID LIB3272-020-P1-K1-E12
Method BLASTX
NCBI GI g2129987
BLAST score 422
E value 1.0e-41
Match length 92
% identity 85
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - potato (fragment) >gi_755187 (U17005) glyceraldehyde 3-phosphate dehydrogenase [Solanum tuberosum]

Seq. No. 233736
Seq. ID LIB3272-020-P1-K1-E2
Method BLASTX
NCBI GI g4263706
BLAST score 343
E value 2.0e-32
Match length 131
% identity 55
NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233737
Seq. ID LIB3272-020-P1-K1-E5
Method BLASTX
NCBI GI g3789799
BLAST score 210
E value 9.0e-17
Match length 127
% identity 9
NCBI Description (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens] >gi_4557445_ref_NP_001259.1_pCHC1L RCC1-like G exchanging factor RLG

E value 3.0e-48
 Match length 130
 % identity 73
 NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I
 chitinase [Gossypium hirsutum]

Seq. No. 233749
 Seq. ID LIB3272-020-P1-K1-G11
 Method BLASTX
 NCBI GI g3659907
 BLAST score 448
 E value 1.0e-44
 Match length 112
 % identity 79
 NCBI Description (AF091857) protein translation factor SUI1 homolog
 [Pimpinella brachycarpa]

Seq. No. 233750
 Seq. ID LIB3272-020-P1-K1-G12
 Method BLASTX
 NCBI GI g1497987
 BLAST score 240
 E value 3.0e-20
 Match length 129
 % identity 40
 NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]

Seq. No. 233751
 Seq. ID LIB3272-020-P1-K1-G3
 Method BLASTX
 NCBI GI g3158376
 BLAST score 485
 E value 5.0e-49
 Match length 129
 % identity 75
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233752
 Seq. ID LIB3272-020-P1-K1-G4
 Method BLASTX
 NCBI GI g3096931
 BLAST score 166
 E value 1.0e-11
 Match length 62
 % identity 52
 NCBI Description (AL023094) putative ribosomal protein S16 [Arabidopsis
 thaliana]

Seq. No. 233753
 Seq. ID LIB3272-020-P1-K1-G5
 Method BLASTX
 NCBI GI g1129145
 BLAST score 551
 E value 9.0e-57
 Match length 134
 % identity 84
 NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No. 233754
 Seq. ID LIB3272-020-P1-K1-G6
 Method BLASTX
 NCBI GI g2583134
 BLAST score 330
 E value 8.0e-31
 Match length 89
 % identity 70
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No. 233755
 Seq. ID LIB3272-020-P1-K1-G7
 Method BLASTX
 NCBI GI g629483
 BLAST score 309
 E value 2.0e-28
 Match length 115
 % identity 56
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula pendula]

Seq. No. 233756
 Seq. ID LIB3272-020-P1-K1-H1
 Method BLASTX
 NCBI GI g4098128
 BLAST score 549
 E value 2.0e-56
 Match length 122
 % identity 89
 NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 233757
 Seq. ID LIB3272-020-P1-K1-H10
 Method BLASTX
 NCBI GI g3551954
 BLAST score 191
 E value 2.0e-14
 Match length 114
 % identity 38
 NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No. 233758
 Seq. ID LIB3272-020-P1-K1-H12
 Method BLASTX
 NCBI GI g4454097
 BLAST score 273
 E value 4.0e-24
 Match length 66
 % identity 82
 NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]

Seq. No. 233759

Seq. ID LIB3272-020-P1-K1-H4
 Method BLASTX
 NCBI GI g4455364
 BLAST score 212
 E value 4.0e-17
 Match length 80
 % identity 51
 NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No. 233760
 Seq. ID LIB3272-020-P1-K1-H8
 Method BLASTX
 NCBI GI g584872
 BLAST score 318
 E value 2.0e-29
 Match length 114
 % identity 49
 NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_629475_pir_S39509
 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - Norway
 spruce >gi_393443_emb_CAA51226_ (X72675) cinnamyl-alcohol
 dehydrogenase [Picea abies] >gi_3451286_emb_CAA05096_
 (AJ001925) cinnamyl alcohol dehydrogenase [Picea abies]
 >gi_3451288_emb_CAA05097_ (AJ001926) cinnamyl alcohol
 dehydrogenase [Picea abies]

Seq. No. 233761
 Seq. ID LIB3272-021-P1-K1-A10
 Method BLASTX
 NCBI GI g2511574
 BLAST score 532
 E value 2.0e-54
 Match length 118
 % identity 93
 NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No. 233762
 Seq. ID LIB3272-021-P1-K1-A11
 Method BLASTX
 NCBI GI g2827559
 BLAST score 156
 E value 2.0e-10
 Match length 42
 % identity 69
 NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
 >gi_3292808_emb_CAA19798_ (AL031018) putative protein
 [Arabidopsis thaliana]

Seq. No. 233763
 Seq. ID LIB3272-021-P1-K1-A12
 Method BLASTX
 NCBI GI g4456760
 BLAST score 482
 E value 1.0e-48
 Match length 110

% identity 73
 NCBI Description (AJ000692) osmotin-like protein [Quercus suber]

Seq. No. 233764
 Seq. ID LIB3272-021-P1-K1-A4
 Method BLASTX
 NCBI GI g2829275
 BLAST score 508
 E value 1.0e-51
 Match length 136
 % identity 73
 NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No. 233765
 Seq. ID LIB3272-021-P1-K1-A5
 Method BLASTX
 NCBI GI g4263791
 BLAST score 270
 E value 9.0e-24
 Match length 133
 % identity 40
 NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 233766
 Seq. ID LIB3272-021-P1-K1-A6
 Method BLASTX
 NCBI GI g729470
 BLAST score 487
 E value 3.0e-49
 Match length 119
 % identity 79
 NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No. 233767
 Seq. ID LIB3272-021-P1-K1-A8
 Method BLASTX
 NCBI GI g3450842
 BLAST score 283
 E value 2.0e-25
 Match length 90
 % identity 59
 NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No. 233768
 Seq. ID LIB3272-021-P1-K1-B1

Method BLASTX
 NCBI GI g2088654
 BLAST score 444
 E value 4.0e-44
 Match length 102
 % identity 84
 NCBI Description (AF002109) 60S acidic ribosomal protein P0 isolog
 [Arabidopsis thaliana]

Seq. No. 233769
 Seq. ID LIB3272-021-P1-K1-B12
 Method BLASTX
 NCBI GI g3643609
 BLAST score 425
 E value 6.0e-42
 Match length 133
 % identity 67
 NCBI Description (AC005395) putative Cys3His zinc finger protein
 [Arabidopsis thaliana]

Seq. No. 233770
 Seq. ID LIB3272-021-P1-K1-B2
 Method BLASTX
 NCBI GI g3342913
 BLAST score 158
 E value 1.0e-10
 Match length 128
 % identity 31
 NCBI Description (AF078916) oligopeptidase B [Trypanosoma brucei brucei]

Seq. No. 233771
 Seq. ID LIB3272-021-P1-K1-B3
 Method BLASTX
 NCBI GI g3913295
 BLAST score 340
 E value 3.0e-32
 Match length 77
 % identity 88
 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
 (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
 3-O-METHYLTRANSFERASE) (COMT) >gi_602588_emb_CAA58218_
 (X83217) caffeic O-methyltransferase [Prunus dulcis]

Seq. No. 233772
 Seq. ID LIB3272-021-P1-K1-B7
 Method BLASTX
 NCBI GI g4426565
 BLAST score 165
 E value 2.0e-11
 Match length 87
 % identity 40
 NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 233773
 Seq. ID LIB3272-021-P1-K1-B8
 Method BLASTX
 NCBI GI g2687584


```
BLAST score      493
E value         6.0e-50
Match length    135
% identity      75
NCBI Description (AF033100) S-adenosylmethionine decarboxylase [Nicotiana
tabacum]
```

```
Seq. No.      233774
Seq. ID      LIB3272-021-P1-K1-C1
Method       BLASTX
NCBI GI      g121953
BLAST score   189
E value      3.0e-14
Match length  43
% identity    88
NCBI Description HISTONE H1 >gi_81905_pir_S00033 histone H1.b - garden pea
               >gi_20762_emb_CAA29123_(X05636) H1 histone (AA 1-263)
               [Pisum sativum]
```

```
Seq. No.      233775
Seq. ID      LIB3272-021-P1-K1-C12
Method       BLASTX
NCBI GI      g1706547
BLAST score   395
E value      8.0e-40
Match length  127
% identity    66
NCBI Description  GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM
                PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE)
                ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE)
                >gi_2129912_pir_S65077 beta-1,3-glucanase class I
                precursor - Para rubber tree >gi_1184668 (U22147)
                beta-1,3-glucanase [Hevea brasiliensis]
```

```
Seq. No.      233776
Seq. ID       LIB3272-021-P1-K1-C3
Method        BLASTX
NCBI GI       g3868758
BLAST score    410
E value        3.0e-40
Match length   77
% identity     94
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
```

```
Seq. No.      233777
Seq. ID      LIB3272-021-P1-K1-C5
Method       BLASTX
NCBI GI      g3694872
BLAST score   429
E value      2.0e-42
Match length  108
% identity    75
NCBI Description (AF092547) profilin [Ricinus communis]
```

```
Seq. No.      233778
Seq. ID      LIB3272-021-P1-K1-C6
Method       BLASTX
```


NCBI GI g2160166
 BLAST score 483
 E value 1.0e-48
 Match length 133
 % identity 66
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233779
 Seq. ID LIB3272-021-P1-K1-C8
 Method BLASTX
 NCBI GI g3242721
 BLAST score 372
 E value 1.0e-35
 Match length 111
 % identity 60
 NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No. 233780
 Seq. ID LIB3272-021-P1-K1-D1
 Method BLASTX
 NCBI GI g2078350
 BLAST score 600
 E value 2.0e-62
 Match length 134
 % identity 87
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 233781
 Seq. ID LIB3272-021-P1-K1-D10
 Method BLASTX
 NCBI GI g3043432
 BLAST score 186
 E value 6.0e-14
 Match length 34
 % identity 100
 NCBI Description (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]

Seq. No. 233782
 Seq. ID LIB3272-021-P1-K1-D11
 Method BLASTX
 NCBI GI g543905
 BLAST score 446
 E value 2.0e-44
 Match length 106
 % identity 82
 NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
 brassinosteroid-regulated protein [Glycine max]

Seq. No. 233783
 Seq. ID LIB3272-021-P1-K1-D3
 Method BLASTX
 NCBI GI g2500354
 BLAST score 648
 E value 3.0e-69
 Match length 134
 % identity 91

Seq. No. 233789
 Seq. ID LIB3272-021-P1-K1-E5
 Method BLASTX
 NCBI GI g3776559
 BLAST score 325
 E value 3.0e-30
 Match length 95
 % identity 64
 NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No. 233790
 Seq. ID LIB3272-021-P1-K1-E7
 Method BLASTX
 NCBI GI g3600058
 BLAST score 328
 E value 1.0e-30
 Match length 90
 % identity 79
 NCBI Description (AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No. 233791
 Seq. ID LIB3272-021-P1-K1-E8
 Method BLASTX
 NCBI GI g3876865
 BLAST score 158
 E value 1.0e-10
 Match length 122
 % identity 36
 NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 233792
 Seq. ID LIB3272-021-P1-K1-F10
 Method BLASTX
 NCBI GI g3702332
 BLAST score 390
 E value 7.0e-38
 Match length 108
 % identity 68
 NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 233793
 Seq. ID LIB3272-021-P1-K1-F11
 Method BLASTX
 NCBI GI g4454043
 BLAST score 338
 E value 7.0e-32
 Match length 112
 % identity 57
 NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Match length	116
% identity	73
NCBI Description	(L08199) peroxidase [<i>Gossypium hirsutum</i>]
Seq. No.	233810
Seq. ID	LIB3272-021-P1-K1-H3
Method	BLASTX
NCBI GI	g267082
BLAST score	559
E value	1.0e-57
Match length	106
% identity	94
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir_JQ1592 tubulin beta-8 chain - <i>Arabidopsis thaliana</i> >gi_166908 (M84705) beta-8 tubulin [<i>Arabidopsis thaliana</i>]
Seq. No.	233811
Seq. ID	LIB3272-021-P1-K1-H4
Method	BLASTX
NCBI GI	g100203
BLAST score	311
E value	1.0e-28
Match length	107
% identity	60
NCBI Description	cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine proteinase [<i>Lycopersicon esculentum</i>]
Seq. No.	233812
Seq. ID	LIB3272-021-P1-K1-H5
Method	BLASTX
NCBI GI	g3643609
BLAST score	428
E value	3.0e-42
Match length	135
% identity	66
NCBI Description	(AC005395) putative Cys3His zinc finger protein [<i>Arabidopsis thaliana</i>]
Seq. No.	233813
Seq. ID	LIB3272-021-P1-K1-H6
Method	BLASTX
NCBI GI	g1279588
BLAST score	411
E value	3.0e-40
Match length	117
% identity	68
NCBI Description	(Z71749) glutathione S-transferase [<i>Nicotiana glauca</i>]
Seq. No.	233814
Seq. ID	LIB3272-021-P1-K1-H7
Method	BLASTX
NCBI GI	g1702983
BLAST score	351
E value	3.0e-33
Match length	110

0000016-101000

>gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738 emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754 emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf_1303352A histone H3 [Helicoverpa zea] >gi_225839_prf_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 233830
Seq. ID LIB3272-022-P1-K1-C5
Method BLASTX
NCBI GI g542200
BLAST score 452
E value 4.0e-45
Match length 125
% identity 66
NCBI Description hypothetical protein - garden asparagus
>gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No. 233831
Seq. ID LIB3272-022-P1-K1-C8
Method BLASTX
NCBI GI g1946355
BLAST score 171
E value 4.0e-12
Match length 58
% identity 53
NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 233832
Seq. ID LIB3272-022-P1-K1-C9
Method BLASTX
NCBI GI g445613
BLAST score 423
E value 1.0e-41
Match length 128
% identity 67
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 233833
Seq. ID LIB3272-022-P1-K1-D11
Method BLASTX
NCBI GI g2499945
BLAST score 355

E value 9.0e-34
 Match length 112
 % identity 62
 NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Arabidopsis thaliana]

Seq. No. 233834
 Seq. ID LIB3272-022-P1-K1-D2
 Method BLASTX
 NCBI GI g1703375
 BLAST score 490
 E value 1.0e-49
 Match length 95
 % identity 100
 NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]

Seq. No. 233835
 Seq. ID LIB3272-022-P1-K1-D3
 Method BLASTX
 NCBI GI g3386621
 BLAST score 592
 E value 2.0e-61
 Match length 126
 % identity 92
 NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 233836
 Seq. ID LIB3272-022-P1-K1-D4
 Method BLASTX
 NCBI GI g3738324
 BLAST score 260
 E value 1.0e-22
 Match length 82
 % identity 55
 NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No. 233837
 Seq. ID LIB3272-022-P1-K1-D5
 Method BLASTX
 NCBI GI g1928981
 BLAST score 474
 E value 1.0e-47
 Match length 114
 % identity 77
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 233838
 Seq. ID LIB3272-022-P1-K1-D6
 Method BLASTX
 NCBI GI g112863

BLAST score	256
E value	4.0e-22
Match length	74
% identity	64
NCBI Description	STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR >gi_100227_pir_S12209 hypothetical protein - tomato >gi_19162_emb_CAA38979_ (X55193) 9612 [Lycopersicon esculentum]
Seq. No.	233839
Seq. ID	LIB3272-022-P1-K1-D8
Method	BLASTX
NCBI GI	g475048
BLAST score	624
E value	3.0e-65
Match length	133
% identity	64
NCBI Description	(X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]
Seq. No.	233840
Seq. ID	LIB3272-022-P1-K1-E11
Method	BLASTX
NCBI GI	g3551247
BLAST score	486
E value	4.0e-49
Match length	144
% identity	68
NCBI Description	(AB012703) 181 [Daucus carota]
Seq. No.	233841
Seq. ID	LIB3272-022-P1-K1-E12
Method	BLASTX
NCBI GI	g3329368
BLAST score	129
E value	3.0e-11
Match length	100
% identity	42
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]
Seq. No.	233842
Seq. ID	LIB3272-022-P1-K1-E3
Method	BLASTX
NCBI GI	g2791834
BLAST score	333
E value	7.0e-35
Match length	127
% identity	67
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.	233843
Seq. ID	LIB3272-022-P1-K1-E4
Method	BLASTX
NCBI GI	g999542
BLAST score	354
E value	1.0e-33
Match length	104

% identity	64
NCBI Description	Spinacia oleracea >gi_999543_pdb_1GYL_B Spinacia oleracea
Seq. No.	233844
Seq. ID	LIB3272-022-P1-K1-E5
Method	BLASTX
NCBI GI	g417719
BLAST score	620
E value	9.0e-65
Match length	140
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_2144763_pir_R3HUS3 ribosomal protein S3 - human >gi_233042_bbs_42659 (S42658) S3 ribosomal protein [human, colon, Peptide, 243 aa] [Homo sapiens] >gi_555941 (U14990) ribosomal protein S3 [Homo sapiens] >gi_555943 (U14991) ribosomal protein S3 [Homo sapiens] >gi_555945 (U14992) ribosomal protein S3 [Homo sapiens]
Seq. No.	233845
Seq. ID	LIB3272-022-P1-K1-E7
Method	BLASTX
NCBI GI	g549063
BLAST score	636
E value	1.0e-66
Match length	144
% identity	83
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]
Seq. No.	233846
Seq. ID	LIB3272-022-P1-K1-E8
Method	BLASTX
NCBI GI	g3608139
BLAST score	353
E value	9.0e-38
Match length	141
% identity	64
NCBI Description	(AC005314) putative fibrillin [Arabidopsis thaliana]
Seq. No.	233847
Seq. ID	LIB3272-022-P1-K1-F1
Method	BLASTX
NCBI GI	g441457
BLAST score	562
E value	5.0e-58
Match length	109
% identity	97
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]
Seq. No.	233848
Seq. ID	LIB3272-022-P1-K1-F10
Method	BLASTX
NCBI GI	g629483

BLAST score 301
 E value 2.0e-27
 Match length 125
 % identity 50
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula
 pendula]

Seq. No. 233849
 Seq. ID LIB3272-022-P1-K1-F11
 Method BLASTX
 NCBI GI g2911044
 BLAST score 369
 E value 2.0e-35
 Match length 118
 % identity 60
 NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 233850
 Seq. ID LIB3272-022-P1-K1-F2
 Method BLASTX
 NCBI GI g1766046
 BLAST score 341
 E value 3.0e-32
 Match length 72
 % identity 86
 NCBI Description (U81993) NAD+ dependent isocitrate dehydrogenase subunit 1
 [Arabidopsis thaliana]

Seq. No. 233851
 Seq. ID LIB3272-022-P1-K1-F3
 Method BLASTX
 NCBI GI g1638842
 BLAST score 390
 E value 7.0e-38
 Match length 93
 % identity 78
 NCBI Description (Z49697) cysteine proteinase inhibitor [Ricinus communis]

Seq. No. 233852
 Seq. ID LIB3272-022-P1-K1-F4
 Method BLASTX
 NCBI GI g629858
 BLAST score 545
 E value 5.0e-56
 Match length 126
 % identity 82
 NCBI Description protein kinase C inhibitor - maize

Seq. No. 233853
 Seq. ID LIB3272-022-P1-K1-F5
 Method BLASTX
 NCBI GI g3980393
 BLAST score 384
 E value 4.0e-37
 Match length 110

09684016-101000

% identity 63
NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 233854
Seq. ID LIB3272-022-P1-K1-F6
Method BLASTX
NCBI GI g3980393
BLAST score 210
E value 6.0e-27
Match length 110
% identity 53
NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 233855
Seq. ID LIB3272-022-P1-K1-F8
Method BLASTX
NCBI GI g3885515
BLAST score 443
E value 5.0e-44
Match length 101
% identity 81
NCBI Description (AF084202) similar to ribosomal protein S26 [Medicago sativa]

Seq. No. 233856
Seq. ID LIB3272-022-P1-K1-G1
Method BLASTX
NCBI GI g3759184
BLAST score 235
E value 1.0e-19
Match length 82
% identity 60
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 233857
Seq. ID LIB3272-022-P1-K1-G10
Method BLASTX
NCBI GI g1931639
BLAST score 237
E value 5.0e-20
Match length 97
% identity 44
NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No. 233858
Seq. ID LIB3272-022-P1-K1-G5
Method BLASTX
NCBI GI g4406816
BLAST score 624
E value 3.0e-65
Match length 123
% identity 93
NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 233859


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Method          BLASTX
NCBI GI         g3935167
BLAST score     229
E value        3.0e-19
Match length    48
% identity      92
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
```

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Seq. No.      233865
Seq. ID       LIB3272-022-P1-K1-H2
Method        BLASTX
NCBI GI       g2673912
BLAST score    200
E value        6.0e-16
Match length   67
% identity     55
NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]
```

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Seq. No.      233866
Seq. ID      LIB3272-023-P1-K1-A1
Method       BLASTX
NCBI GI      g1351014
BLAST score   439
E value      1.0e-43
Match length  107
% identity    83
NCBI Description  40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)
               ribosomal protein S8 [Oryza sativa]
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Seq. No.      233867
Seq. ID      LIB3272-023-P1-K1-A10
Method       BLASTX
NCBI GI      g462147
BLAST score   698
E value      6.0e-74
Match length  138
% identity    95
NCBI Description  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
                  (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                  (PHI) >gi_541866_pir_S41808 glucose-6-phosphate isomerase
                  (EC 5.3.1.9) - Arabidopsis thaliana
                  >gi_415923_emb_CAA48940_(X69195) glucose-6-phosphate
                  isomerase [Arabidopsis thaliana]
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Seq. No.	233868
Seq. ID	LIB3272-023-P1-K1-A12
Method	BLASTX
NCBI GI	g4538929
BLAST score	319
E value	2.0e-29
Match length	118
% identity	43
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No. 233869
Seq. ID LIB3272-023-P1-K1-A3

NCBI Description (X92489) homeobox-leucine zipper protein [Glycine max]

Seq. No. 233890
 Seq. ID LIB3272-023-P1-K1-D7
 Method BLASTX
 NCBI GI g3914430
 BLAST score 743
 E value 3.0e-79
 Match length 145
 % identity 98
 NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
 >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No. 233891
 Seq. ID LIB3272-023-P1-K1-D8
 Method BLASTX
 NCBI GI g3068809
 BLAST score 536
 E value 6.0e-55
 Match length 127
 % identity 83
 NCBI Description (AF059295) Skp1 homolog [Arabidopsis thaliana]

Seq. No. 233892
 Seq. ID LIB3272-023-P1-K1-D9
 Method BLASTX
 NCBI GI g3157951
 BLAST score 201
 E value 8.0e-17
 Match length 86
 % identity 67
 NCBI Description (AC002131) Contains similarity to vesicle trafficking protein gb_U91538 from Mus musculus. ESTs gb_F15494 and gb_F14097 come from this gene. [Arabidopsis thaliana]

Seq. No. 233893
 Seq. ID LIB3272-023-P1-K1-E12
 Method BLASTX
 NCBI GI g1172002
 BLAST score 591
 E value 2.0e-61
 Match length 143
 % identity 76
 NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_556424 (L36822)
 phenylalanine ammonia lyase [Stylosanthes humilis]

Seq. No. 233894
 Seq. ID LIB3272-023-P1-K1-E2
 Method BLASTX
 NCBI GI g2462931
 BLAST score 157
 E value 2.0e-10
 Match length 88
 % identity 50
 NCBI Description (Z83833) UDP-glucose:sterol glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 233895
Seq. ID LIB3272-023-P1-K1-E3
Method BLASTX
NCBI GI g2586127
BLAST score 363
E value 1.0e-34
Match length 138
% identity 52
NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No. 233896
Seq. ID LIB3272-023-P1-K1-E4
Method BLASTX
NCBI GI g2507421
BLAST score 451
E value 6.0e-45
Match length 95
% identity 91
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
(U81042) translation initiation factor [Arabidopsis
thaliana] >gi_4490709_emb_CAB38843.1 (AL035680)
translation initiation factor [Arabidopsis thaliana]

Seq. No. 233897
Seq. ID LIB3272-023-P1-K1-E6
Method BLASTX
NCBI GI g131015
BLAST score 470
E value 4.0e-47
Match length 123
% identity 68
NCBI Description PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR
(THAUMATIN-LIKE PROTEIN E22) >gi_100385_pir_JH0230
pathogenesis-related protein R precursor - common tobacco
>gi_19855_emb_CAA33293 (X15224) thaumatin-like protein
[Nicotiana tabacum] >gi_19980_emb_CAA31235 (X12739)
pathogenesis-related protein R (AA 1 - 226) [Nicotiana
tabacum]

Seq. No. 233898
Seq. ID LIB3272-023-P1-K1-E7
Method BLASTX
NCBI GI g2213583
BLAST score 468
E value 6.0e-47
Match length 126
% identity 73
NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No. 233899
Seq. ID LIB3272-023-P1-K1-E8
Method BLASTX
NCBI GI g2651303
BLAST score 531
E value 2.0e-54

00684016-101000

BLAST score 217
E value 8.0e-18
Match length 66
% identity 62
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248
pyruvate kinase (EC 2.7.1.40) - potato
>gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
tuberosum]

Seq. No. 233927
Seq. ID LIB3272-024-P1-K1-A8
Method BLASTX
NCBI GI g167367
BLAST score 196
E value 4.0e-28
Match length 115
% identity 68
NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 233928
Seq. ID LIB3272-024-P1-K1-A9
Method BLASTX
NCBI GI g508304
BLAST score 207
E value 2.0e-16
Match length 51
% identity 78
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233929
Seq. ID LIB3272-024-P1-K1-B1
Method BLASTX
NCBI GI g542058
BLAST score 497
E value 2.0e-50
Match length 131
% identity 68
NCBI Description HSR203J protein - common tobacco >gi_444002_emb_CAA54393_
(X77136) HSR203J [Nicotiana tabacum]

Seq. No. 233930
Seq. ID LIB3272-024-P1-K1-B12
Method BLASTX
NCBI GI g575603
BLAST score 324
E value 4.0e-30
Match length 109
% identity 57
NCBI Description (D42064) cationic peroxidase isozyme 38K precursor
[Nicotiana tabacum]

Seq. No. 233931
Seq. ID LIB3272-024-P1-K1-B2
Method BLASTX
NCBI GI g464986
BLAST score 523
E value 2.0e-53

40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 233936
 Seq. ID LIB3272-024-P1-K1-B7
 Method BLASTX
 NCBI GI g629483
 BLAST score 331
 E value 7.0e-31
 Match length 125
 % identity 54
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula
 pendula]

Seq. No. 233937
 Seq. ID LIB3272-024-P1-K1-B8
 Method BLASTX
 NCBI GI g3158376
 BLAST score 488
 E value 2.0e-49
 Match length 131
 % identity 75
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233938
 Seq. ID LIB3272-024-P1-K1-C1
 Method BLASTX
 NCBI GI g2252836
 BLAST score 300
 E value 2.0e-27
 Match length 86
 % identity 67
 NCBI Description (AF013293) contains weak similarity to S. cerevisiae BOB1
 protein (PIR:S45444) [Arabidopsis thaliana]

Seq. No. 233939
 Seq. ID LIB3272-024-P1-K1-C2
 Method BLASTX
 NCBI GI g1730109
 BLAST score 475
 E value 7.0e-48
 Match length 112
 % identity 82
 NCBI Description LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
 HYDROXYLASE) >gi_499022_emb_CAA53580_ (X75966)
 leucoanthocyanidin dioxygenase [Vitis vinifera]

Seq. No. 233940
 Seq. ID LIB3272-024-P1-K1-C4
 Method BLASTX
 NCBI GI g3980393
 BLAST score 399
 E value 7.0e-39
 Match length 122
 % identity 61
 NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis

0908-7614

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Seq. No.      233942
Seq. ID       LIB3272-024-P1-K1-D11
Method        BLASTX
NCBI GI       g4510430
BLAST score   518
E value       8.0e-53
Match length  108
% identity    86
NCBI Description (AC006929) unknown protein, 3' partial [Arabidopsis
thaliana]
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Seq. No.                239344
Seq. ID                 LIB3272-024-P1-K1-D3
Method                  BLASTX
NCBI GI                 g464707
BLAST score             570
E value                 6.0e-59
Match length            116
% identity               96
NCBI Description        40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
                        protein S18.A - Arabidopsis thaliana
                        >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                        [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                        S18 ribosomal protein [Arabidopsis thaliana]
                        >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                        [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                        S18 ribosomal protein [Arabidopsis thaliana]
                        >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                        [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                        ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                        thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                        gb_R30430 come from this gene. [Arabidopsis thaliana]
                        >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                        protein [Arabidopsis thaliana]

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Seq. No.	233945
Seq. ID	LIB3272-024-P1-K1-D5
Method	BLASTX
NCBI GI	g2529683
BLAST score	343
E value	2.0e-32
Match length	129
% identity	57
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]
Seq. No.	233946
Seq. ID	LIB3272-024-P1-K1-D6
Method	BLASTX
NCBI GI	g2791804
BLAST score	186
E value	6.0e-14
Match length	62
% identity	58
NCBI Description	(AF041432) bet3 [Homo sapiens] >gi_3413800_emb_CAA11902_ (AJ224335) hBET3 protein [Homo sapiens]
Seq. No.	233947
Seq. ID	LIB3272-024-P1-K1-D9
Method	BLASTX
NCBI GI	g1408471
BLAST score	468
E value	6.0e-47
Match length	106
% identity	79
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]
Seq. No.	233948
Seq. ID	LIB3272-024-P1-K1-E10
Method	BLASTX
NCBI GI	g464981
BLAST score	465
E value	1.0e-46
Match length	87
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.	233949
Seq. ID	LIB3272-024-P1-K1-E12
Method	BLASTX
NCBI GI	g2501578
BLAST score	502
E value	2.0e-55
Match length	124
% identity	97
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir_S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

NCBI GI g3913413
 BLAST score 268
 E value 2.0e-23
 Match length 58
 % identity 90
 NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 1 (ADOMETDC 1) (SAMDC 1) (SAMDC9) >gi_1155240 (U38526)
 S-adenosylmethionine decarboxylase 1 [Dianthus caryophyllus] >gi_2406585 (U94786) S-adenosylmethionine decarboxylase [Dianthus caryophyllus]

Seq. No. 233955
 Seq. ID LIB3272-024-P1-K1-E8
 Method BLASTX
 NCBI GI g1168727
 BLAST score 386
 E value 2.0e-37
 Match length 105
 % identity 67
 NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol dehydrogenase [Aralia cordata] >gi_745086_prf_2015401A cinnamoyl alcohol dehydrogenase [Aralia cordata]

Seq. No. 233956
 Seq. ID LIB3272-024-P1-K1-E9
 Method BLASTX
 NCBI GI g2129739
 BLAST score 302
 E value 1.0e-27
 Match length 70
 % identity 89
 NCBI Description shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947) shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No. 233957
 Seq. ID LIB3272-024-P1-K1-F10
 Method BLASTX
 NCBI GI g2760837
 BLAST score 199
 E value 2.0e-15
 Match length 89
 % identity 40
 NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 233958
 Seq. ID LIB3272-024-P1-K1-F11
 Method BLASTX
 NCBI GI g4314355
 BLAST score 323
 E value 6.0e-30
 Match length 97
 % identity 59
 NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	233959
Seq. ID	LIB3272-024-P1-K1-F2
Method	BLASTX
NCBI GI	g3850778
BLAST score	434
E value	5.0e-43
Match length	106
% identity	76
NCBI Description	(Y18346) gluaredoxin [<i>Lycopersicon esculentum</i>]
Seq. No.	233960
Seq. ID	LIB3272-024-P1-K1-F5
Method	BLASTX
NCBI GI	g120669
BLAST score	476
E value	6.0e-48
Match length	105
% identity	86
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - <i>Magnolia liliiflora</i> >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [<i>Magnolia liliiflora</i>]
Seq. No.	233961
Seq. ID	LIB3272-024-P1-K1-F6
Method	BLASTX
NCBI GI	g4567249
BLAST score	509
E value	9.0e-52
Match length	133
% identity	68
NCBI Description	(AC007070) hypothetical protein [<i>Arabidopsis thaliana</i>]
Seq. No.	233962
Seq. ID	LIB3272-024-P1-K1-F7
Method	BLASTX
NCBI GI	g585241
BLAST score	165
E value	2.0e-11
Match length	64
% identity	56
NCBI Description	HISTONE H1 >gi_629668_pir_S45662 histone H1 - tomato >gi_424100 (U03391) histone H1 [<i>Lycopersicon esculentum</i>]
Seq. No.	233963
Seq. ID	LIB3272-024-P1-K1-G10
Method	BLASTX
NCBI GI	g1076660
BLAST score	526
E value	9.0e-54
Match length	135
% identity	78
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [<i>Solanum tuberosum</i> =potatoes, leaf, Peptide, 342 aa] [<i>Solanum tuberosum</i>]

Seq. No.	233964
Seq. ID	LIB3272-024-P1-K1-G2
Method	BLASTX
NCBI GI	g2253411
BLAST score	194
E value	8.0e-15
Match length	65
% identity	48
NCBI Description	(AF007219) PP2A inhibitor [Tetraodon fluviatilis]
Seq. No.	233965
Seq. ID	LIB3272-024-P1-K1-G3
Method	BLASTX
NCBI GI	g1922938
BLAST score	220
E value	8.0e-18
Match length	129
% identity	36
NCBI Description	(AC000106) Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb_Z29094). [Arabidopsis thaliana]
Seq. No.	233966
Seq. ID	LIB3272-024-P1-K1-G5
Method	BLASTX
NCBI GI	g2267567
BLAST score	403
E value	2.0e-39
Match length	87
% identity	87
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]
Seq. No.	233967
Seq. ID	LIB3272-024-P1-K1-G6
Method	BLASTX
NCBI GI	g3023847
BLAST score	555
E value	4.0e-57
Match length	116
% identity	35
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]
Seq. No.	233968
Seq. ID	LIB3272-024-P1-K1-G7
Method	BLASTX
NCBI GI	g2129915
BLAST score	299
E value	4.0e-27
Match length	97
% identity	61
NCBI Description	ferredoxin precursor - sweet orange >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic ferredoxin [Citrus sinensis]

Seq. No.	233969
Seq. ID	LIB3272-024-P1-K1-G8
Method	BLASTX
NCBI GI	g1762933
BLAST score	458
E value	9.0e-46
Match length	116
% identity	78
NCBI Description	(U66263) tumor-related protein [Nicotiana tabacum]
Seq. No.	233970
Seq. ID	LIB3272-024-P1-K1-G9
Method	BLASTX
NCBI GI	g2832708
BLAST score	280
E value	6.0e-25
Match length	107
% identity	50
NCBI Description	(AL021713) beta-1, 3-glucanase-like protein [Arabidopsis thaliana]
Seq. No.	233971
Seq. ID	LIB3272-024-P1-K1-H10
Method	BLASTX
NCBI GI	g1706326
BLAST score	497
E value	2.0e-50
Match length	114
% identity	82
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_2146786_pir_S65470 pyruvate decarboxylase (EC 4.1.1.1) (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_ (Z66543) pyruvate decarboxylase [Pisum sativum]
Seq. No.	233972
Seq. ID	LIB3272-024-P1-K1-H3
Method	BLASTX
NCBI GI	g267082
BLAST score	620
E value	9.0e-65
Match length	119
% identity	95
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir_JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]
Seq. No.	233973
Seq. ID	LIB3272-024-P1-K1-H4
Method	BLASTX
NCBI GI	g131385
BLAST score	542
E value	1.0e-55
Match length	134
% identity	84
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

09664016 - 101000

33792

E value 2.0e-20
 Match length 114
 % identity 47
 NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No. 233979
 Seq. ID LIB3272-026-P1-K1-A9
 Method BLASTX
 NCBI GI g2984709
 BLAST score 402
 E value 3.0e-39
 Match length 82
 % identity 91
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 233980
 Seq. ID LIB3272-026-P1-K1-B1
 Method BLASTX
 NCBI GI g2984709
 BLAST score 468
 E value 6.0e-47
 Match length 97
 % identity 90
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 233981
 Seq. ID LIB3272-026-P1-K1-B10
 Method BLASTX
 NCBI GI g1166450
 BLAST score 294
 E value 1.0e-26
 Match length 63
 % identity 83
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

Seq. No. 233982
 Seq. ID LIB3272-026-P1-K1-B12
 Method BLASTX
 NCBI GI g4481934
 BLAST score 163
 E value 3.0e-11
 Match length 105
 % identity 14
 NCBI Description (AL035640) CDA peptide synthetase I [Streptomyces coelicolor]

Seq. No. 233983
 Seq. ID LIB3272-026-P1-K1-B3
 Method BLASTX
 NCBI GI g3319921
 BLAST score 242
 E value 2.0e-20
 Match length 94
 % identity 57
 NCBI Description (AJ223388) Hev b 3 [Hevea brasiliensis]

Seq. ID LIB3272-026-P1-K1-C5
Method BLASTX
NCBI GI g2146797
BLAST score 442
E value 5.0e-44
Match length 116
% identity 43
NCBI Description protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
>gi_1134968 (U41385) protein disulphide isomerase PDI
[Ricinus communis] >gi_1587210_prf_2206331A protein
disulfide isomerase [Ricinus communis]

Seq. No. 233990
Seq. ID LIB3272-026-P1-K1-D12
Method BLASTX
NCBI GI g4538967
BLAST score 302
E value 2.0e-27
Match length 80
% identity 72
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
thaliana]

Seq. No. 233991
Seq. ID LIB3272-026-P1-K1-D4
Method BLASTX
NCBI GI g3158474
BLAST score 581
E value 3.0e-60
Match length 122
% identity 92
NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 233992
Seq. ID LIB3272-026-P1-K1-D5
Method BLASTX
NCBI GI g119640
BLAST score 176
E value 6.0e-13
Match length 78
% identity 51
NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
E8) >gi_82109_pir_S01642 ripening protein E8 - tomato
>gi_19199_emb_CAA31789_ (X13437) E8 protein [Lycopersicon
esculentum]

Seq. No. 233993
Seq. ID LIB3272-026-P1-K1-E1
Method BLASTX
NCBI GI g3309084
BLAST score 386
E value 2.0e-37
Match length 88
% identity 89
NCBI Description (AF076252) calcineurin B-like protein 2 [Arabidopsis
thaliana]

Seq. ID LIB3272-026-P1-K1-G7
 Method BLASTX
 NCBI GI g1710780
 BLAST score 397
 E value 6.0e-39
 Match length 98
 % identity 77
 NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No. 234005
 Seq. ID LIB3272-026-P1-K1-H1
 Method BLASTX
 NCBI GI g417148
 BLAST score 345
 E value 1.0e-32
 Match length 122
 % identity 55
 NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir_A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No. 234006
 Seq. ID LIB3272-026-P1-K1-H10
 Method BLASTX
 NCBI GI g3776577
 BLAST score 199
 E value 2.0e-15
 Match length 95
 % identity 42
 NCBI Description (AC005388) T22H22.24 [Arabidopsis thaliana]

Seq. No. 234007
 Seq. ID LIB3272-026-P1-K1-H11
 Method BLASTX
 NCBI GI g2347189
 BLAST score 341
 E value 4.0e-32
 Match length 84
 % identity 79
 NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana] >gi_3150399 (AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No. 234008
 Seq. ID LIB3272-026-P1-K1-H9
 Method BLASTX
 NCBI GI g267069
 BLAST score 336
 E value 9.0e-32
 Match length 70
 % identity 87
 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) alpha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 234009
 Seq. ID LIB3272-027-P1-K1-A10
 Method BLASTX
 NCBI GI g2648355
 BLAST score 148
 E value 2.0e-09
 Match length 138
 % identity 32
 NCBI Description (AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]

Seq. No. 234010
 Seq. ID LIB3272-027-P1-K1-A2
 Method BLASTX
 NCBI GI g1362055
 BLAST score 360
 E value 3.0e-34
 Match length 79
 % identity 90
 NCBI Description phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - alfalfa >gi_603221 (U18239) 6-phosphogluconate dehydrogenase [Medicago sativa subsp. sativa]

Seq. No. 234011
 Seq. ID LIB3272-027-P1-K1-A4
 Method BLASTX
 NCBI GI g132944
 BLAST score 653
 E value 1.0e-68
 Match length 128
 % identity 93
 NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir_JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 234012
 Seq. ID LIB3272-027-P1-K1-A5
 Method BLASTX
 NCBI GI g4371284
 BLAST score 678
 E value 1.0e-71
 Match length 142
 % identity 91
 NCBI Description (AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No. 234013
 Seq. ID LIB3272-027-P1-K1-A6
 Method BLASTX
 NCBI GI g547712
 BLAST score 695
 E value 1.0e-73
 Match length 143
 % identity 95
 NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir_S38358 translation initiation factor eIF-4A

- rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic
initiation factor 4A [Oryza sativa]

Seq. No. 234014
Seq. ID LIB3272-027-P1-K1-A7
Method BLASTX
NCBI GI g3868758
BLAST score 420
E value 2.0e-41
Match length 105
% identity 73
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 234015
Seq. ID LIB3272-027-P1-K1-B2
Method BLASTX
NCBI GI g1352681
BLAST score 217
E value 2.0e-17
Match length 117
% identity 48
NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir_S55457
phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
thaliana >gi_633028_dbj_BAA07287_ (D38109) protein
phosphatase 2C [Arabidopsis thaliana]

Seq. No. 234016
Seq. ID LIB3272-027-P1-K1-B4
Method BLASTX
NCBI GI g2129670
BLAST score 450
E value 8.0e-45
Match length 132
% identity 65
NCBI Description phosphoinositide-specific phospholipase C - Arabidopsis
thaliana >gi_857374_dbj_BAA09432_ (D50804) phosphoinositide
specific phospholipase C [Arabidopsis thaliana]

Seq. No. 234017
Seq. ID LIB3272-027-P1-K1-B8
Method BLASTX
NCBI GI g3413511
BLAST score 553
E value 6.0e-57
Match length 137
% identity 80
NCBI Description (AJ000265) glucose-6-phosphate isomerase [Spinacia
oleracea]

Seq. No. 234018
Seq. ID LIB3272-027-P1-K1-B9
Method BLASTX
NCBI GI g2274915
BLAST score 410
E value 4.0e-40
Match length 113
% identity 69

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NCBI Description (AJ000081) beta-1,3-glucanase [Citrus sinensis]

Seq. No. 234019
Seq. ID LIB3272-027-P1-K1-C1
Method BLASTX
NCBI GI g122770
BLAST score 442
E value 5.0e-44
Match length 112
% identity 79
NCBI Description HEMOGLOBIN II >gi_99509_pir_S13378 hemoglobin II - swamp
oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina
glauca]

Seq. No. 234020
Seq. ID LIB3272-027-P1-K1-C11
Method BLASTX
NCBI GI g267075
BLAST score 751
E value 4.0e-80
Match length 144
% identity 95
NCBI Description TUBULIN BETA-2 CHAIN >gi_388254_emb_CAA38614_ (X54845)
beta-tubulin 2 [Pisum sativum]

Seq. No. 234021
Seq. ID LIB3272-027-P1-K1-C2
Method BLASTX
NCBI GI g167367
BLAST score 139
E value 2.0e-19
Match length 86
% identity 69
NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 234022
Seq. ID LIB3272-027-P1-K1-C3
Method BLASTX
NCBI GI g3881978
BLAST score 325
E value 4.0e-30
Match length 83
% identity 46
NCBI Description (Y11348) annexin-like protein [Medicago sativa]

Seq. No. 234023
Seq. ID LIB3272-027-P1-K1-C6
Method BLASTX
NCBI GI g2388575
BLAST score 239
E value 4.0e-20
Match length 133
% identity 39
NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 234024
Seq. ID LIB3272-027-P1-K1-D11

>gi_488605_emb_CAA55854_ (X79267) allergen [Betula pendula]

Seq. No. 234029
 Seq. ID LIB3272-027-P1-K1-D6
 Method BLASTX
 NCBI GI g4210948
 BLAST score 473
 E value 2.0e-47
 Match length 94
 % identity 94
 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 234030
 Seq. ID LIB3272-027-P1-K1-D7
 Method BLASTX
 NCBI GI g3643602
 BLAST score 263
 E value 5.0e-23
 Match length 103
 % identity 54
 NCBI Description (AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No. 234031
 Seq. ID LIB3272-027-P1-K1-D8
 Method BLASTX
 NCBI GI g3023186
 BLAST score 535
 E value 8.0e-55
 Match length 131
 % identity 79
 NCBI Description 14-3-3-LIKE PROTEIN 9 >gi_1771180_emb_CAA67373.1_ (X98865)
 14-3-3 protein [Lycopersicon esculentum]

Seq. No. 234032
 Seq. ID LIB3272-027-P1-K1-E1
 Method BLASTX
 NCBI GI g3023281
 BLAST score 379
 E value 2.0e-36
 Match length 105
 % identity 70
 NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER
 >gi_2065194_emb_CAA64475_ (X95098) ammonium transporter
 [Lycopersicon esculentum]

Seq. No. 234033
 Seq. ID LIB3272-027-P1-K1-E10
 Method BLASTX
 NCBI GI g1279654
 BLAST score 384
 E value 4.0e-37
 Match length 108
 % identity 71
 NCBI Description (X97351) peroxidase [Populus balsamifera subsp.
 trichocarpa]


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Seq. No.      234034
Seq. ID      LIB3272-027-P1-K1-E5
Method       BLASTX
NCBI GI      g2244806
BLAST score   277
E value      2.0e-24
Match length  88
% identity   59
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
```

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Seq. No.      234035
Seq. ID      LIB3272-027-P1-K1-E6
Method       BLASTX
NCBI GI      g1729971
BLAST score   270
E value      1.0e-23
Match length  69
% identity   70
NCBI Description  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein -
                rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                sativa]
```

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Seq. No.      234036
Seq. ID      LIB3272-027-P1-K1-E7
Method       BLASTX
NCBI GI      g3789911
BLAST score   156
E value      2.0e-10
Match length  87
% identity    40
NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium
discoideum]
```

```
Seq. No.      234037
Seq. ID      LIB3272-027-P1-K1-E8
Method       BLASTX
NCBI GI      g1707018
BLAST score   212
E value      2.0e-17
Match length  55
% identity    75
NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]
```

```
Seq. No.      234038
Seq. ID       LIB3272-027-P1-K1-F1
Method        BLASTX
NCBI GI       g992706
BLAST score    543
E value        9.0e-56
Match length   105
% identity     91
NCBI Description (U33758) UBC13 [Arabidopsis thaliana]
```

Seq. No.	234039
Seq. ID	LIB3272-027-P1-K1-F10
Method	BLASTX

Seq. ID LIB3272-028-P1-K1-A11
 Method BLASTX
 NCBI GI g4006850
 BLAST score 434
 E value 5.0e-43
 Match length 133
 % identity 60
 NCBI Description (Z99707) cytochrome like protein [Arabidopsis thaliana]

Seq. No. 234061
 Seq. ID LIB3272-028-P1-K1-A12
 Method BLASTX
 NCBI GI g416649
 BLAST score 383
 E value 5.0e-37
 Match length 119
 % identity 64
 NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT1/PCNT110) >gi_100303_pir_S16267 auxin-induced protein (clone pGNT1) - common tobacco >gi_19789_emb_CAA39709_ (X56268) auxin-induced protein [Nicotiana tabacum] >gi_19795_emb_CAA39705_ (X56264) auxin-induced protein [Nicotiana tabacum]

Seq. No. 234062
 Seq. ID LIB3272-028-P1-K1-A2
 Method BLASTX
 NCBI GI g416664
 BLAST score 149
 E value 1.0e-09
 Match length 37
 % identity 78
 NCBI Description PLASMA MEMBRANE ATPASE 4 (PROTON PUMP) >gi_485504_pir_S33548 H+-transporting ATPase (EC 3.6.1.35) type 4, plasma membrane - curled-leaved tobacco >gi_19704_emb_CAA47275_ (X66737) plasma membrane H+-ATPase [Nicotiana plumbaginifolia]

Seq. No. 234063
 Seq. ID LIB3272-028-P1-K1-A3
 Method BLASTX
 NCBI GI g3360289
 BLAST score 384
 E value 4.0e-37
 Match length 139
 % identity 55
 NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No. 234064
 Seq. ID LIB3272-028-P1-K1-A4
 Method BLASTX
 NCBI GI g1657948
 BLAST score 460
 E value 5.0e-46
 Match length 120
 % identity 76

NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]
Seq. No.	234065
Seq. ID	LIB3272-028-P1-K1-A5
Method	BLASTX
NCBI GI	g4417279
BLAST score	477
E value	5.0e-48
Match length	134
% identity	67
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]
Seq. No.	234066
Seq. ID	LIB3272-028-P1-K1-A6
Method	BLASTX
NCBI GI	g1703375
BLAST score	643
E value	2.0e-67
Match length	127
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420) DcARF1 [Daucus carota]
Seq. No.	234067
Seq. ID	LIB3272-028-P1-K1-A7
Method	BLASTX
NCBI GI	g4056457
BLAST score	527
E value	7.0e-54
Match length	126
% identity	79
NCBI Description	(AC005990) ESTs gb_234051 and gb_F13722 come from this gene. [Arabidopsis thaliana]
Seq. No.	234068
Seq. ID	LIB3272-028-P1-K1-A9
Method	BLASTX
NCBI GI	g508304
BLAST score	261
E value	9.0e-23
Match length	61
% identity	80
NCBI Description	(L22305) corC [Medicago sativa]
Seq. No.	234069
Seq. ID	LIB3272-028-P1-K1-B10
Method	BLASTX
NCBI GI	g2911042
BLAST score	352
E value	2.0e-33
Match length	91
% identity	78
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
Seq. No.	234070
Seq. ID	LIB3272-028-P1-K1-B11

NCBI GI g4104242
 BLAST score 632
 E value 3.0e-66
 Match length 137
 % identity 87
 NCBI Description (AF034266) palmitoyl-acyl carrier protein thioesterase
 [Gossypium hirsutum]

Seq. No. 234086
 Seq. ID LIB3272-028-P1-K1-D3
 Method BLASTX
 NCBI GI g2129726
 BLAST score 560
 E value 9.0e-58
 Match length 120
 % identity 87
 NCBI Description RNA polymerase II third largest chain RPB35.5A -
 Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II
 third largest subunit [Arabidopsis thaliana]
 >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA
 polymerase II, third largest subunit [Arabidopsis thaliana]

Seq. No. 234087
 Seq. ID LIB3272-028-P1-K1-D5
 Method BLASTX
 NCBI GI g4261517
 BLAST score 361
 E value 2.0e-34
 Match length 85
 % identity 78
 NCBI Description (AF117334) cysteine proteinase inhibitor [Ipomoea batatas]

Seq. No. 234088
 Seq. ID LIB3272-028-P1-K1-D7
 Method BLASTX
 NCBI GI g2129915
 BLAST score 507
 E value 1.0e-51
 Match length 131
 % identity 72
 NCBI Description ferredoxin precursor - sweet orange
 >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic
 ferredoxin [Citrus sinensis]

Seq. No. 234089
 Seq. ID LIB3272-028-P1-K1-D8
 Method BLASTX
 NCBI GI g1850546
 BLAST score 407
 E value 8.0e-40
 Match length 104
 % identity 79
 NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis
 thaliana]

Seq. No. 234090
 Seq. ID LIB3272-028-P1-K1-D9


```
BLAST score      515
E value          2.0e-52
Match length     112
% identity       83
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
>gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
[Arabidopsis thaliana]
```

```
Seq. No.      234096
Seq. ID       LIB3272-028-P1-K1-E7
Method        BLASTX
NCBI GI       g167367
BLAST score   464
E value       1.0e-46
Match length  120
% identity    76
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
```

```
Seq. No.      234097
Seq. ID      LIB3272-028-P1-K1-E9
Method       BLASTX
NCBI GI      g3915031
BLAST score   700
E value      3.0e-74
Match length  132
% identity    99
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_
                (X95988) delta 9 stearyl-[acyl-carrier protein] desaturase
                [Gossypium hirsutum]
```

```
Seq. No.      234098
Seq. ID      LIB3272-028-P1-K1-F1
Method       BLASTX
NCBI GI      g2129579
BLAST score   748
E value      8.0e-80
Match length  136
% identity    94
NCBI Description Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
              Dwarf1 [Arabidopsis thaliana]
```

```
Seq. No.          234099
Seq. ID           LIB3272-028-P1-K1-F4
Method            BLASTX
NCBI GI           g20186
BLAST score       491
E value           1.0e-49
Match length      96
% identity        55
NCBI Description   (X65016) calmodulin [Oryza sativa]
                  >gi_3336950_emb_CAA74307_ (Y13974) calmodulin [Zea mays]
                  >gi_4103961 (AF030034) calmodulin [Phaseolus vulgaris]
```

Seq. No. 234100
Seq. ID LIB3272-028-P1-K1-F5

Method BLASTX
 NCBI GI g464986
 BLAST score 522
 E value 3.0e-53
 Match length 96
 % identity 99
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 234101
 Seq. ID LIB3272-028-P1-K1-F6
 Method BLASTX
 NCBI GI g2924521
 BLAST score 183
 E value 1.0e-13
 Match length 109
 % identity 43
 NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

Seq. No. 234102
 Seq. ID LIB3272-028-P1-K1-F7
 Method BLASTX
 NCBI GI g585241
 BLAST score 193
 E value 1.0e-14
 Match length 98
 % identity 45
 NCBI Description HISTONE H1 >gi_629668_pir_S45662 histone H1 - tomato
 >gi_424100 (U03391) histone H1 [Lycopersicon esculentum]

Seq. No. 234103
 Seq. ID LIB3272-028-P1-K1-F9
 Method BLASTX
 NCBI GI g1841870
 BLAST score 344
 E value 2.0e-32
 Match length 93
 % identity 75
 NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]

Seq. No. 234104
 Seq. ID LIB3272-028-P1-K1-G11
 Method BLASTX
 NCBI GI g2829896
 BLAST score 395
 E value 2.0e-38
 Match length 133
 % identity 56

E value 1.0e-46
 Match length 110
 % identity 76
 NCBI Description (Z70677) thioredoxin [Ricinus communis]

Seq. No. 234121
 Seq. ID LIB3272-029-P1-K1-C1
 Method BLASTX
 NCBI GI g1076389
 BLAST score 495
 E value 4.0e-50
 Match length 108
 % identity 92
 NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana
 >gi_683502_emb_CAA57528 (X82002) protein phosphatase 2A 65
 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 234122
 Seq. ID LIB3272-029-P1-K1-C12
 Method BLASTX
 NCBI GI g1174592
 BLAST score 497
 E value 2.0e-50
 Match length 96
 % identity 94
 NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
 - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
 sativum] .

Seq. No. 234123
 Seq. ID LIB3272-029-P1-K1-C2
 Method BLASTX
 NCBI GI g629483
 BLAST score 326
 E value 3.0e-30
 Match length 125
 % identity 54
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696 (X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
 pendula]

Seq. No. 234124
 Seq. ID LIB3272-029-P1-K1-C3
 Method BLASTX
 NCBI GI g3759184
 BLAST score 202
 E value 7.0e-16
 Match length 105
 % identity 51
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 234125
 Seq. ID LIB3272-029-P1-K1-C4
 Method BLASTX
 NCBI GI g3334147
 BLAST score 613

E value 6.0e-64
 Match length 142
 % identity 84
 NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I
 chitinase [Gossypium hirsutum]

Seq. No. 234126
 Seq. ID LIB3272-029-P1-K1-C8
 Method BLASTX
 NCBI GI g3608136
 BLAST score 231
 E value 2.0e-35
 Match length 89
 % identity 90
 NCBI Description (AC005314) defender against cell death [Arabidopsis
 thaliana]

Seq. No. 234127
 Seq. ID LIB3272-029-P1-K1-D10
 Method BLASTX
 NCBI GI g3377813
 BLAST score 190
 E value 2.0e-14
 Match length 61
 % identity 57
 NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]

Seq. No. 234128
 Seq. ID LIB3272-029-P1-K1-D2
 Method BLASTX
 NCBI GI g3158376
 BLAST score 151
 E value 5.0e-16
 Match length 121
 % identity 50
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 234129
 Seq. ID LIB3272-029-P1-K1-D3
 Method BLASTX
 NCBI GI g4467153
 BLAST score 483
 E value 1.0e-48
 Match length 104
 % identity 82
 NCBI Description (AL035540) putative thaumatin-like protein [Arabidopsis
 thaliana]

Seq. No. 234130
 Seq. ID LIB3272-029-P1-K1-D4
 Method BLASTX
 NCBI GI g2501555
 BLAST score 315
 E value 5.0e-29
 Match length 114
 % identity 54
 NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148)

% identity 67
NCBI Description (L34773) RNA polymerase subunit [Arabidopsis thaliana]
>gi_2462755 (AC002292) RNA polymerase subunit (isoform B)
[Arabidopsis thaliana] >gi_1586550_prf_2204246B RNA
polymerase [Arabidopsis thaliana]

Seq. No. 234142
Seq. ID LIB3272-029-P1-K1-F1
Method BLASTX
NCBI GI g300264
BLAST score 248
E value 3.0e-21
Match length 98
% identity 58
NCBI Description (S59747) HSP68=68 kda heat-stress DnaK homolog [Solanum
tuberosum=potatoes, Peptide Mitochondrial, 682 aa] [Solanum
tuberosum]

Seq. No. 234143
Seq. ID LIB3272-029-P1-K1-F10
Method BLASTX
NCBI GI g2369766
BLAST score 389
E value 1.0e-37
Match length 126
% identity 62
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No. 234144
Seq. ID LIB3272-029-P1-K1-F11
Method BLASTX
NCBI GI g2498885
BLAST score 142
E value 7.0e-18
Match length 113
% identity 49
NCBI Description PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A
>gi_1296664_emb_CAA65774_ (X97064) Sec23 protein [Homo
sapiens]

Seq. No. 234145
Seq. ID LIB3272-029-P1-K1-F12
Method BLASTX
NCBI GI g3915031
BLAST score 713
E value 1.0e-75
Match length 137
% identity 98
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
(STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_
(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
[Gossypium hirsutum]

Seq. No. 234146
Seq. ID LIB3272-029-P1-K1-F5
Method BLASTX
NCBI GI g464986

BLAST score 427
 E value 3.0e-42
 Match length 91
 % identity 88
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 234147
 Seq. ID LIB3272-029-P1-K1-F8
 Method BLASTX
 NCBI GI g1778376
 BLAST score 519
 E value 6.0e-53
 Match length 141
 % identity 68
 NCBI Description (U81288) PsRT17-1 [Pisum sativum]

Seq. No. 234148
 Seq. ID LIB3272-029-P1-K1-G1
 Method BLASTX
 NCBI GI g445612
 BLAST score 208
 E value 1.0e-16
 Match length 90
 % identity 52
 NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 234149
 Seq. ID LIB3272-029-P1-K1-G10
 Method BLASTX
 NCBI GI g2501449
 BLAST score 398
 E value 9.0e-39
 Match length 78
 % identity 97
 NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi_1668773_emb_CAA67922_ (X99608) ubiquitin-like protein [Oryza sativa]

Seq. No. 234150
 Seq. ID LIB3272-029-P1-K1-G12
 Method BLASTX
 NCBI GI g120669
 BLAST score 489
 E value 2.0e-49
 Match length 104
 % identity 89
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate

E value 5.0e-22
 Match length 84
 % identity 62
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 234161
 Seq. ID LIB3272-029-P1-K1-H2
 Method BLASTX
 NCBI GI g167367
 BLAST score 640
 E value 4.0e-67
 Match length 138
 % identity 91
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 234162
 Seq. ID LIB3272-029-P1-K1-H4
 Method BLASTX
 NCBI GI g3600039
 BLAST score 283
 E value 8.0e-49
 Match length 140
 % identity 68
 NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No. 234163
 Seq. ID LIB3272-029-P1-K1-H7
 Method BLASTX
 NCBI GI g2921512
 BLAST score 455
 E value 2.0e-45
 Match length 112
 % identity 83
 NCBI Description (AF037460) GF14 protein [Fritillaria agrestis]

Seq. No. 234164
 Seq. ID LIB3272-030-P1-K1-A1
 Method BLASTX
 NCBI GI g1705812
 BLAST score 449
 E value 1.0e-44
 Match length 136
 % identity 62
 NCBI Description ACIDIC CHITINASE PRECURSOR >gi_1150686_emb_CAA92207_ (Z68123) acidic chitinase [Vitis vinifera]

Seq. No. 234165
 Seq. ID LIB3272-030-P1-K1-A10
 Method BLASTX
 NCBI GI g2347098
 BLAST score 512
 E value 4.0e-52
 Match length 107
 % identity 93
 NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific

protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 234166
 Seq. ID LIB3272-030-P1-K1-A11
 Method BLASTX
 NCBI GI g2924521
 BLAST score 178
 E value 5.0e-13
 Match length 109
 % identity 43
 NCBI Description (AL022023) putative protein [Arabidopsis thaliana]

Seq. No. 234167
 Seq. ID LIB3272-030-P1-K1-A12
 Method BLASTX
 NCBI GI g2078350
 BLAST score 604
 E value 6.0e-63
 Match length 134
 % identity 90
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 234168
 Seq. ID LIB3272-030-P1-K1-A2
 Method BLASTX
 NCBI GI g4539457
 BLAST score 198
 E value 3.0e-15
 Match length 55
 % identity 65
 NCBI Description (AL049500) heat shock transcription factor-like protein [Arabidopsis thaliana]

Seq. No. 234169
 Seq. ID LIB3272-030-P1-K1-A5
 Method BLASTX
 NCBI GI g1848212
 BLAST score 451
 E value 5.0e-45
 Match length 87
 % identity 44
 NCBI Description (Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]

Seq. No. 234170
 Seq. ID LIB3272-030-P1-K1-A7
 Method BLASTX
 NCBI GI g3249066
 BLAST score 381
 E value 9.0e-37
 Match length 128
 % identity 66
 NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein gb_984964. ESTs gb_F15433 and gb_AA395158 come from this gene. [Arabidopsis thaliana]

Seq. No. 234171

Method BLASTX
 NCBI GI g4521249
 BLAST score 433
 E value 6.0e-43
 Match length 114
 % identity 74
 NCBI Description (AB013912) DNA helicase [Mus musculus]

Seq. No. 234182
 Seq. ID LIB3272-030-P1-K1-C7
 Method BLASTX
 NCBI GI g1169009
 BLAST score 684
 E value 3.0e-72
 Match length 134
 % identity 90
 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
 (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
 3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir_S40146
 catechol O-methyltransferase (EC 2.1.1.6) - cider tree
 >gi_437777_emb_CAA52814_ (X74814) O-Methyltransferase
 [Eucalyptus gunnii]

Seq. No. 234183
 Seq. ID LIB3272-030-P1-K1-C8
 Method BLASTX
 NCBI GI g2244740
 BLAST score 167
 E value 9.0e-12
 Match length 44
 % identity 75
 NCBI Description (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No. 234184
 Seq. ID LIB3272-030-P1-K1-D10
 Method BLASTX
 NCBI GI g404670
 BLAST score 385
 E value 3.0e-37
 Match length 130
 % identity 59
 NCBI Description (L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934
 (AC003970) phytochrome A [Arabidopsis thaliana]

Seq. No. 234185
 Seq. ID LIB3272-030-P1-K1-D11
 Method BLASTX
 NCBI GI g3237190
 BLAST score 144
 E value 3.0e-09
 Match length 56
 % identity 54
 NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus]

Seq. No. 234186
 Seq. ID LIB3272-030-P1-K1-D12
 Method BLASTX

NCBI GI g2541876
 BLAST score 159
 E value 8.0e-11
 Match length 79
 % identity 49
 NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No. 234187
 Seq. ID LIB3272-030-P1-K1-D5
 Method BLASTX
 NCBI GI g4371284
 BLAST score 565
 E value 2.0e-58
 Match length 125
 % identity 86
 NCBI Description (AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No. 234188
 Seq. ID LIB3272-030-P1-K1-D8
 Method BLASTX
 NCBI GI g4115377
 BLAST score 270
 E value 9.0e-24
 Match length 85
 % identity 69
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 234189
 Seq. ID LIB3272-030-P1-K1-E12
 Method BLASTX
 NCBI GI g3763925
 BLAST score 332
 E value 4.0e-31
 Match length 70
 % identity 87
 NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No. 234190
 Seq. ID LIB3272-030-P1-K1-E2
 Method BLASTX
 NCBI GI g585973
 BLAST score 499
 E value 1.0e-50
 Match length 123
 % identity 83
 NCBI Description FRUCTOKINASE >gi_626018_pir_S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283 (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf_2108342A fructokinase [Solanum tuberosum]

Seq. No. 234191
 Seq. ID LIB3272-030-P1-K1-E3
 Method BLASTX
 NCBI GI g3128177
 BLAST score 486

% identity	22
NCBI Description	calmodulin [Chlamydomonas reinhardtii]
Seq. No.	234197
Seq. ID	LIB3272-030-P1-K1-F7
Method	BLASTX
NCBI GI	g3128228
BLAST score	626
E value	2.0e-65
Match length	128
% identity	91
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]
Seq. No.	234198
Seq. ID	LIB3272-030-P1-K1-F8
Method	BLASTX
NCBI GI	g167367
BLAST score	328
E value	1.0e-30
Match length	82
% identity	77
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]
Seq. No.	234199
Seq. ID	LIB3272-030-P1-K1-F9
Method	BLASTX
NCBI GI	g125887
BLAST score	194
E value	5.0e-15
Match length	102
% identity	46
NCBI Description	ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR >gi_82092_pir_S04765 LAT52 protein precursor - tomato >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon esculentum]
Seq. No.	234200
Seq. ID	LIB3272-030-P1-K1-G11
Method	BLASTX
NCBI GI	g217909
BLAST score	328
E value	1.0e-30
Match length	74
% identity	88
NCBI Description	(D14044) glycolate oxidase [Cucurbita sp.]
Seq. No.	234201
Seq. ID	LIB3272-030-P1-K1-G3
Method	BLASTX
NCBI GI	g3212854
BLAST score	272
E value	5.0e-24
Match length	126
% identity	59
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

09584016-101000

Method BLASTX
 NCBI GI g862931
 BLAST score 356
 E value 6.0e-34
 Match length 106
 % identity 69
 NCBI Description (U27179) acidic glucanase [Medicago sativa subsp. sativa]

Seq. No. 234208
 Seq. ID LIB3272-030-P1-K1-H10
 Method BLASTX
 NCBI GI g136057
 BLAST score 177
 E value 3.0e-13
 Match length 59
 % identity 61
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_99499_pir_A32187 (S)-tetrahydroberberine oxidase -
 Coptis japonica >gi_556171 (J04121) triosephosphate
 isomerase [Coptis japonica]

Seq. No. 234209
 Seq. ID LIB3272-030-P1-K1-H12
 Method BLASTX
 NCBI GI g2440044
 BLAST score 319
 E value 8.0e-30
 Match length 65
 % identity 91
 NCBI Description (AJ001293) major intrinsic protein PIPB [Craterostigma
 plantagineum]

Seq. No. 234210
 Seq. ID LIB3272-030-P1-K1-H2
 Method BLASTX
 NCBI GI g1928981
 BLAST score 537
 E value 4.0e-55
 Match length 114
 % identity 93
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
 oleracea var. botrytis]

Seq. No. 234211
 Seq. ID LIB3272-030-P1-K1-H3
 Method BLASTX
 NCBI GI g2829871
 BLAST score 129
 E value 4.0e-09
 Match length 93
 % identity 44
 NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 234212
 Seq. ID LIB3272-030-P1-K1-H9
 Method BLASTX
 NCBI GI g1107526

BLAST score 235
 E value 6.0e-20
 Match length 70
 % identity 61
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 234213
 Seq. ID LIB3272-031-P1-K1-A10
 Method BLASTX
 NCBI GI g1653767
 BLAST score 434
 E value 5.0e-43
 Match length 134
 % identity 59
 NCBI Description (D90916) oligopeptidase A [Synechocystis sp.]

Seq. No. 234214
 Seq. ID LIB3272-031-P1-K1-A3
 Method BLASTX
 NCBI GI g131385
 BLAST score 438
 E value 2.0e-43
 Match length 130
 % identity 70
 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
 SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
 THYLAKOID MEMBRANE PROTEIN)

Seq. No. 234215
 Seq. ID LIB3272-031-P1-K1-A4
 Method BLASTX
 NCBI GI g548852
 BLAST score 361
 E value 2.0e-34
 Match length 82
 % identity 80
 NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal
 protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
 subunit ribosomal protein [Oryza sativa]

Seq. No. 234216
 Seq. ID LIB3272-031-P1-K1-A7
 Method BLASTX
 NCBI GI g1709498
 BLAST score 514
 E value 2.0e-52
 Match length 129
 % identity 74
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 234217
 Seq. ID LIB3272-031-P1-K1-B12
 Method BLASTX
 NCBI GI g3158376

BLAST score 442
 E value 6.0e-44
 Match length 120
 % identity 75
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 234218
 Seq. ID LIB3272-031-P1-K1-B3
 Method BLASTX
 NCBI GI g3319882
 BLAST score 518
 E value 8.0e-53
 Match length 139
 % identity 76
 NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
 arietinum]

Seq. No. 234219
 Seq. ID LIB3272-031-P1-K1-B4
 Method BLASTX
 NCBI GI g3869088
 BLAST score 643
 E value 2.0e-67
 Match length 123
 % identity 100
 NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No. 234220
 Seq. ID LIB3272-031-P1-K1-B5
 Method BLASTX
 NCBI GI g3288821
 BLAST score 422
 E value 1.0e-48
 Match length 123
 % identity 80
 NCBI Description (AF063901) alanine:glyoxylate aminotransferase;
 transaminase [Arabidopsis thaliana]

Seq. No. 234221
 Seq. ID LIB3272-031-P1-K1-B6
 Method BLASTX
 NCBI GI g1172995
 BLAST score 238
 E value 5.0e-20
 Match length 95
 % identity 54
 NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir_S52084 ribosomal
 protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
 ribosomal protein L22 [Rattus norvegicus]
 >gi_1093952_prf_2105193A ribosomal protein L22 [Rattus
 norvegicus]

Seq. No. 234222
 Seq. ID LIB3272-031-P1-K1-B7
 Method BLASTX
 NCBI GI g1170747
 BLAST score 361

NCBI GI g2738248
 BLAST score 508
 E value 1.0e-51
 Match length 138
 % identity 76
 NCBI Description (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No. 234228
 Seq. ID LIB3272-031-P1-K1-C6
 Method BLASTX
 NCBI GI g3980393
 BLAST score 262
 E value 6.0e-27
 Match length 102
 % identity 64
 NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No. 234229
 Seq. ID LIB3272-031-P1-K1-D1
 Method BLASTX
 NCBI GI g2388689
 BLAST score 217
 E value 2.0e-17
 Match length 84
 % identity 55
 NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 234230
 Seq. ID LIB3272-031-P1-K1-D12
 Method BLASTX
 NCBI GI g1657948
 BLAST score 385
 E value 2.0e-37
 Match length 104
 % identity 74
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 234231
 Seq. ID LIB3272-031-P1-K1-D2
 Method BLASTX
 NCBI GI g4049354
 BLAST score 689
 E value 7.0e-73
 Match length 137
 % identity 96
 NCBI Description (AL034567) glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein [Arabidopsis thaliana]

Seq. No. 234232
 Seq. ID LIB3272-031-P1-K1-D3
 Method BLASTX
 NCBI GI g2213597
 BLAST score 317
 E value 3.0e-29
 Match length 86

% identity	71
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]
Seq. No.	234233
Seq. ID	LIB3272-031-P1-K1-D4
Method	BLASTX
NCBI GI	g728880
BLAST score	181
E value	2.0e-13
Match length	98
% identity	43
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]
Seq. No.	234234
Seq. ID	LIB3272-031-P1-K1-D5
Method	BLASTX
NCBI GI	g495725
BLAST score	603
E value	8.0e-63
Match length	133
% identity	85
NCBI Description	(L25042) acetyl-CoA carboxylase [Medicago sativa]
Seq. No.	234235
Seq. ID	LIB3272-031-P1-K1-D6
Method	BLASTX
NCBI GI	g123620
BLAST score	552
E value	6.0e-57
Match length	114
% identity	96
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950 heat shock cognate protein 70 - tomato >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate 70 [Lycopersicon esculentum]
Seq. No.	234236
Seq. ID	LIB3272-031-P1-K1-E1
Method	BLASTX
NCBI GI	g3702332
BLAST score	199
E value	2.0e-24
Match length	98
% identity	66
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.	234237
Seq. ID	LIB3272-031-P1-K1-E10
Method	BLASTX
NCBI GI	g167367
BLAST score	542
E value	9.0e-56
Match length	119
% identity	89

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No. 234243
 Seq. ID LIB3272-031-P1-K1-F11
 Method BLASTX
 NCBI GI g3913996
 BLAST score 422
 E value 1.0e-41
 Match length 119
 % identity 70

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR
 >gi_2208927_dbj_BAA20482_ (D85610) ATP-dependent protease Lon [Spinacia oleracea]

Seq. No. 234244
 Seq. ID LIB3272-031-P1-K1-F2
 Method BLASTX
 NCBI GI g2267567
 BLAST score 391
 E value 6.0e-38
 Match length 87
 % identity 85

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No. 234245
 Seq. ID LIB3272-031-P1-K1-F3
 Method BLASTX
 NCBI GI g2982311
 BLAST score 250
 E value 2.0e-21
 Match length 92
 % identity 59

NCBI Description (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]

Seq. No. 234246
 Seq. ID LIB3272-031-P1-K1-F4
 Method BLASTX
 NCBI GI g2811025
 BLAST score 202
 E value 1.0e-19
 Match length 90
 % identity 61

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_ (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 234247
 Seq. ID LIB3272-031-P1-K1-F5
 Method BLASTX
 NCBI GI g2507421
 BLAST score 467
 E value 7.0e-47
 Match length 97

% identity 63
 NCBI Description (L36159) unknown protein [Medicago sativa]

Seq. No. 234253
 Seq. ID LIB3272-031-P1-K1-G6
 Method BLASTX
 NCBI GI g3845257
 BLAST score 161
 E value 5.0e-11
 Match length 100
 % identity 6
 NCBI Description (AE001413) predicted integral membrane protein [Plasmodium falciparum]

Seq. No. 234254
 Seq. ID LIB3272-031-P1-K1-G7
 Method BLASTX
 NCBI GI g3142698
 BLAST score 509
 E value 9.0e-52
 Match length 137
 % identity 68
 NCBI Description (AF064542) protein farnesyltransferase subunit A [Arabidopsis thaliana]

Seq. No. 234255
 Seq. ID LIB3272-031-P1-K1-H1
 Method BLASTX
 NCBI GI g322750
 BLAST score 151
 E value 3.0e-11
 Match length 77
 % identity 56
 NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]

Seq. No. 234256
 Seq. ID LIB3272-031-P1-K1-H12
 Method BLASTX
 NCBI GI g4539459
 BLAST score 400
 E value 5.0e-39
 Match length 114
 % identity 67
 NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 234257
 Seq. ID LIB3272-031-P1-K1-H2
 Method BLASTX
 NCBI GI g3123515
 BLAST score 663
 E value 8.0e-70
 Match length 136
 % identity 93
 NCBI Description (Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. ID LIB3272-032-P1-K1-A11
 Method BLASTX
 NCBI GI g3882081
 BLAST score 521
 E value 3.0e-53
 Match length 108
 % identity 36
 NCBI Description (AJ012552) polyubiquitin [Vicia faba]

Seq. No. 234264
 Seq. ID LIB3272-032-P1-K1-A12
 Method BLASTX
 NCBI GI g4539292
 BLAST score 461
 E value 3.0e-46
 Match length 95
 % identity 88
 NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 234265
 Seq. ID LIB3272-032-P1-K1-A3
 Method BLASTX
 NCBI GI g1408471
 BLAST score 437
 E value 2.0e-43
 Match length 98
 % identity 79
 NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No. 234266
 Seq. ID LIB3272-032-P1-K1-A5
 Method BLASTX
 NCBI GI g3033380
 BLAST score 442
 E value 6.0e-44
 Match length 112
 % identity 76
 NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No. 234267
 Seq. ID LIB3272-032-P1-K1-A6
 Method BLASTX
 NCBI GI g3046700
 BLAST score 211
 E value 4.0e-17
 Match length 65
 % identity 66
 NCBI Description (AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi_4191787 (AC005917) putative cytidine deaminase [Arabidopsis thaliana]

Seq. No. 234268

NCBI GI g2583134
 BLAST score 179
 E value 3.0e-13
 Match length 105
 % identity 46
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis thaliana]

Seq. No. 234274
 Seq. ID LIB3272-032-P1-K1-C10
 Method BLASTX
 NCBI GI g1199772
 BLAST score 344
 E value 2.0e-32
 Match length 119
 % identity 62
 NCBI Description (D83226) extensin like protein [Populus nigra]
 >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein [Populus nigra]

Seq. No. 234275
 Seq. ID LIB3272-032-P1-K1-C11
 Method BLASTX
 NCBI GI g1107526
 BLAST score 413
 E value 1.0e-40
 Match length 119
 % identity 66
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 234276
 Seq. ID LIB3272-032-P1-K1-C2
 Method BLASTX
 NCBI GI g1928981
 BLAST score 485
 E value 5.0e-49
 Match length 109
 % identity 89
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 234277
 Seq. ID LIB3272-032-P1-K1-C3
 Method BLASTX
 NCBI GI g4115337
 BLAST score 394
 E value 3.0e-38
 Match length 82
 % identity 16
 NCBI Description (L81141) ubiquitin [Pisum sativum]

Seq. No. 234278
 Seq. ID LIB3272-032-P1-K1-C5
 Method BLASTX
 NCBI GI g543867
 BLAST score 374
 E value 6.0e-36

Seq. No. 234293
 Seq. ID LIB3272-032-P1-K1-E3
 Method BLASTX
 NCBI GI g401189
 BLAST score 513
 E value 3.0e-52
 Match length 109
 % identity 89
 NCBI Description WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP) (TURGOR-RESPONSIVE PROTEIN 7A) >gi_485511_pir_S33617 trg-31 protein - garden pea >gi_20426_emb_CAA79159_ (Z18288) trg-31 [Pisum sativum]

Seq. No. 234294
 Seq. ID LIB3272-032-P1-K1-E4
 Method BLASTX
 NCBI GI g1076660
 BLAST score 188
 E value 4.0e-14
 Match length 47
 % identity 79
 NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 234295
 Seq. ID LIB3272-032-P1-K1-E9
 Method BLASTX
 NCBI GI g3646373
 BLAST score 596
 E value 5.0e-62
 Match length 116
 % identity 93
 NCBI Description (AJ011078) RGP1 protein [Oryza sativa]

Seq. No. 234296
 Seq. ID LIB3272-032-P1-K1-F11
 Method BLASTX
 NCBI GI g3759184
 BLAST score 285
 E value 2.0e-25
 Match length 125
 % identity 50
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 234297
 Seq. ID LIB3272-032-P1-K1-F12
 Method BLASTX
 NCBI GI g4454097
 BLAST score 277
 E value 1.0e-24
 Match length 67
 % identity 82
 NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]

Seq. No. 234298

Seq. ID LIB3272-032-P1-K1-F2
 Method BLASTX
 NCBI GI g1709498
 BLAST score 377
 E value 2.0e-36
 Match length 85
 % identity 80
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 234299
 Seq. ID LIB3272-032-P1-K1-F3
 Method BLASTX
 NCBI GI g2791834
 BLAST score 509
 E value 3.0e-52
 Match length 111
 % identity 96
 NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No. 234300
 Seq. ID LIB3272-032-P1-K1-F5
 Method BLASTX
 NCBI GI g2507281
 BLAST score 634
 E value 2.0e-66
 Match length 114
 % identity 99
 NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
 (X97380) atran2 [Arabidopsis thaliana]

Seq. No. 234301
 Seq. ID LIB3272-032-P1-K1-F7
 Method BLASTX
 NCBI GI g3915165
 BLAST score 484
 E value 5.0e-49
 Match length 106
 % identity 89
 NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi_2792520
 (AF042320) tryptophan synthase beta subunit [Camptotheca
 acuminata] >gi_2801771 (AF042321) tryptophan synthase beta
 [Camptotheca acuminata]

Seq. No. 234302
 Seq. ID LIB3272-032-P1-K1-F8
 Method BLASTX
 NCBI GI g3860333
 BLAST score 392
 E value 4.0e-38
 Match length 99
 % identity 69
 NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No. 234303

Seq. No.	234308
Seq. ID	LIB3272-032-P1-K1-G7
Method	BLASTX
NCBI GI	g1001312
BLAST score	270
E value	8.0e-24
Match length	84
% identity	63
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]
Seq. No.	234309
Seq. ID	LIB3272-032-P1-K1-G9
Method	BLASTX
NCBI GI	g549063
BLAST score	140
E value	7.0e-09
Match length	69
% identity	51
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]
Seq. No.	234310
Seq. ID	LIB3272-032-P1-K1-H1
Method	BLASTX
NCBI GI	g441457
BLAST score	290
E value	3.0e-26
Match length	65
% identity	80
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]
Seq. No.	234311
Seq. ID	LIB3272-032-P1-K1-H11
Method	BLASTX
NCBI GI	g3687243
BLAST score	235
E value	9.0e-20
Match length	59
% identity	78
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]
Seq. No.	234312
Seq. ID	LIB3272-032-P1-K1-H2
Method	BLASTX
NCBI GI	g2501578
BLAST score	489
E value	1.0e-49
Match length	104
% identity	95
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir_S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No. 234313
 Seq. ID LIB3272-032-P1-K1-H5
 Method BLASTX
 NCBI GI g2894599
 BLAST score 533
 E value 1.0e-54
 Match length 115
 % identity 81
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 234314
 Seq. ID LIB3272-032-P1-K1-H6
 Method BLASTX
 NCBI GI g2842486
 BLAST score 331
 E value 6.0e-31
 Match length 105
 % identity 65
 NCBI Description (AL021749) putative protein [Arabidopsis thaliana]

Seq. No. 234315
 Seq. ID LIB3272-032-P1-K1-H8
 Method BLASTX
 NCBI GI g3868758
 BLAST score 412
 E value 2.0e-40
 Match length 99
 % identity 77
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 234316
 Seq. ID LIB3272-033-P1-K1-A1
 Method BLASTX
 NCBI GI g4210948
 BLAST score 470
 E value 3.0e-47
 Match length 99
 % identity 91
 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 234317
 Seq. ID LIB3272-033-P1-K1-A10
 Method BLASTX
 NCBI GI g3023190
 BLAST score 278
 E value 9.0e-25
 Match length 95
 % identity 64
 NCBI Description 14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685)
 14-3-3 protein [Solanum tuberosum]

Seq. No. 234318
 Seq. ID LIB3272-033-P1-K1-A11
 Method BLASTX
 NCBI GI g1431629
 BLAST score 352

E value 2.0e-33
 Match length 95
 % identity 68
 NCBI Description (X99348) pectinacetylerase precursor [Vigna radiata].

Seq. No. 234319
 Seq. ID LIB3272-033-P1-K1-A2
 Method BLASTX
 NCBI GI g3158376
 BLAST score 425
 E value 6.0e-42
 Match length 118
 % identity 74
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 234320
 Seq. ID LIB3272-033-P1-K1-A4
 Method BLASTX
 NCBI GI g2583108
 BLAST score 227
 E value 9.0e-19
 Match length 91
 % identity 55
 NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 234321
 Seq. ID LIB3272-033-P1-K1-A5
 Method BLASTX
 NCBI GI g464986
 BLAST score 469
 E value 4.0e-47
 Match length 87
 % identity 98
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 234322
 Seq. ID LIB3272-033-P1-K1-A6
 Method BLASTX
 NCBI GI g1666234
 BLAST score 551
 E value 8.0e-57
 Match length 103
 % identity 98
 NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No. 234323

BLAST score 179
E. value 4.0e-13
Match length 111
% identity 46
NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 234334
Seq. ID LIB3272-033-P1-K1-C4
Method BLASTX
NCBI GI g1076393
BLAST score 360
E value 2.0e-34
Match length 94
% identity 80
NCBI Description RCI14A protein - Arabidopsis thaliana
>gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No. 234335
Seq. ID LIB3272-033-P1-K1-C5
Method BLASTX
NCBI GI g4097579
BLAST score 513
E value 3.0e-52
Match length 105
% identity 91
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 234336
Seq. ID LIB3272-033-P1-K1-C7
Method BLASTX
NCBI GI g4510376
BLAST score 205
E value 3.0e-16
Match length 69
% identity 55
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 234337
Seq. ID LIB3272-033-P1-K1-C8
Method BLASTX
NCBI GI g122770
BLAST score 443
E value 4.0e-44
Match length 112
% identity 79
NCBI Description HEMOGLOBIN II >gi_99509_pir_S13378 hemoglobin II - swamp oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina glauca]

Seq. No. 234338
Seq. ID LIB3272-033-P1-K1-C9
Method BLASTX
NCBI GI g3879192
BLAST score 274
E value 3.0e-24

Match length 123
 % identity 48
 NCBI Description (Z50795) weak similarity with yeast cat8 regulatory protein (Swiss Prot accession number P39113); cDNA EST EMBL:Z14554 comes from this gene; cDNA EST EMBL:T02057 comes from this gene; cDNA EST EMBL:D75504 comes from this gene;

Seq. No. 234339
 Seq. ID LIB3272-033-P1-K1-D1
 Method BLASTX
 NCBI GI g3236242
 BLAST score 439
 E value 1.0e-43
 Match length 103
 % identity 84
 NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 234340
 Seq. ID LIB3272-033-P1-K1-D10
 Method BLASTX
 NCBI GI g3522945
 BLAST score 263
 E value 5.0e-23
 Match length 116
 % identity 44
 NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 234341
 Seq. ID LIB3272-033-P1-K1-D11
 Method BLASTX
 NCBI GI g4126401
 BLAST score 420
 E value 2.0e-41
 Match length 95
 % identity 85
 NCBI Description (AB011795) flavanone 3-hydroxylase [Citrus sinensis]

Seq. No. 234342
 Seq. ID LIB3272-033-P1-K1-D2
 Method BLASTX
 NCBI GI g549063
 BLAST score 447
 E value 1.0e-44
 Match length 103
 % identity 82
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP). >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No. 234343
 Seq. ID LIB3272-033-P1-K1-D4
 Method BLASTX
 NCBI GI g445613
 BLAST score 400
 E value 5.0e-39

E value 2.0e-56
 Match length 114
 % identity 95
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 234360
 Seq. ID LIB3272-033-P1-K1-G4
 Method BLASTX
 NCBI GI g1352461
 BLAST score 491
 E value 1.0e-49
 Match length 113
 % identity 81
 NCBI Description IN2-2 PROTEIN

Seq. No. 234361
 Seq. ID LIB3272-033-P1-K1-G5
 Method BLASTX
 NCBI GI g3885884
 BLAST score 538
 E value 3.0e-55
 Match length 105
 % identity 92
 NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 234362
 Seq. ID LIB3272-033-P1-K1-G6
 Method BLASTX
 NCBI GI g1694621
 BLAST score 329
 E value 9.0e-31
 Match length 102
 % identity 67
 NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No. 234363
 Seq. ID LIB3272-033-P1-K1-G7
 Method BLASTX
 NCBI GI g3834310
 BLAST score 466
 E value 8.0e-47
 Match length 89
 % identity 100
 NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No. 234364
 Seq. ID LIB3272-033-P1-K1-G8
 Method BLASTX
 NCBI GI g3176662
 BLAST score 497
 E value 2.0e-50
 Match length 121
 % identity 71

Seq. ID LIB3272-034-P1-K1-A4
 Method BLASTX
 NCBI GI g3386615
 BLAST score 157
 E value 1.0e-10
 Match length 54
 % identity 63
 NCBI Description (AC004665) putative phosphomannomutase [Arabidopsis thaliana]

Seq. No. 234371
 Seq. ID LIB3272-034-P1-K1-A5
 Method BLASTX
 NCBI GI g3395431
 BLAST score 209
 E value 1.0e-16
 Match length 76
 % identity 49
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 234372
 Seq. ID LIB3272-034-P1-K1-A7
 Method BLASTX
 NCBI GI g549063
 BLAST score 211
 E value 4.0e-17
 Match length 70
 % identity 63
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1072464_pir_A38958 IgE-dependent histamine-releasing
 factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
 21kd polypeptide [Oryza sativa]

Seq. No. 234373
 Seq. ID LIB3272-034-P1-K1-A9
 Method BLASTX
 NCBI GI g419789
 BLAST score 482
 E value 1.0e-48
 Match length 121
 % identity 79
 NCBI Description hypothetical protein - potato

Seq. No. 234374
 Seq. ID LIB3272-034-P1-K1-B1
 Method BLASTX
 NCBI GI g3914430
 BLAST score 491
 E value 8.0e-50
 Match length 98
 % identity 97
 NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
 CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
 >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta
 subunit [Spinacia oleracea]

Seq. No. 234375

Seq. ID LIB3272-034-P1-K1-B12
 Method BLASTX
 NCBI GI g2088654
 BLAST score 433
 E value 7.0e-43
 Match length 97
 % identity 87
 NCBI Description (AF002109) 60S acidic ribosomal protein P0 isolog
 [Arabidopsis thaliana]

Seq. No. 234376
 Seq. ID LIB3272-034-P1-K1-B5
 Method BLASTX
 NCBI GI g1107526
 BLAST score 491
 E value 1.0e-49
 Match length 122
 % identity 75
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 234377
 Seq. ID LIB3272-034-P1-K1-B6
 Method BLASTX
 NCBI GI g1166450
 BLAST score 161
 E value 3.0e-11
 Match length 33
 % identity 88
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

Seq. No. 234378
 Seq. ID LIB3272-034-P1-K1-B9
 Method BLASTX
 NCBI GI g927025
 BLAST score 339
 E value 6.0e-32
 Match length 77
 % identity 55
 NCBI Description (L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No. 234379
 Seq. ID LIB3272-034-P1-K1-C1
 Method BLASTX
 NCBI GI g3242720
 BLAST score 185
 E value 8.0e-14
 Match length 54
 % identity 61
 NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
 thaliana]

Seq. No. 234380
 Seq. ID LIB3272-034-P1-K1-C10
 Method BLASTX
 NCBI GI g4406780
 BLAST score 405
 E value 1.0e-39

Match length 111
 % identity 68
 NCBI Description (AC006532) putative multispanning membrane protein
 [Arabidopsis thaliana]

 Seq. No. 234381
 Seq. ID LIB3272-034-P1-K1-C12
 Method BLASTX
 NCBI GI g1709498
 BLAST score 491
 E value 1.0e-49
 Match length 107
 % identity 82
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 234382
 Seq. ID LIB3272-034-P1-K1-C3
 Method BLASTX
 NCBI GI g3522937
 BLAST score 329
 E value 1.0e-30
 Match length 69
 % identity 83
 NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 234383
 Seq. ID LIB3272-034-P1-K1-C4
 Method BLASTX
 NCBI GI g629602
 BLAST score 157
 E value 1.0e-10
 Match length 48
 % identity 65
 NCBI Description probable imbibition protein - wild cabbage
 >gi_488787_emb_CAA55893_ (X79330) putative imbibition
 protein [Brassica oleracea]

Seq. No. 234384
 Seq. ID LIB3272-034-P1-K1-C6
 Method BLASTX
 NCBI GI g730536
 BLAST score 247
 E value 2.0e-29
 Match length 74
 % identity 93
 NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal
 protein subunit L17 [Nicotiana tabacum]

Seq. No. 234385
 Seq. ID LIB3272-034-P1-K1-C7
 Method BLASTX
 NCBI GI g2274915
 BLAST score 299
 E value 2.0e-27

thaliana]

Seq. No. 234391
 Seq. ID LIB3272-034-P1-K1-D4
 Method BLASTX
 NCBI GI g3334147
 BLAST score 500
 E value 9.0e-51
 Match length 126
 % identity 78
 NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I
 chitinase [Gossypium hirsutum]

Seq. No. 234392
 Seq. ID LIB3272-034-P1-K1-D7
 Method BLASTX
 NCBI GI g2879867
 BLAST score 396
 E value 1.0e-38
 Match length 106
 % identity 71
 NCBI Description (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
 pombe]

Seq. No. 234393
 Seq. ID LIB3272-034-P1-K1-D8
 Method BLASTX
 NCBI GI g508304
 BLAST score 244
 E value 9.0e-21
 Match length 58
 % identity 79
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 234394
 Seq. ID LIB3272-034-P1-K1-E12
 Method BLASTX
 NCBI GI g1173209
 BLAST score 633
 E value 2.0e-66
 Match length 129
 % identity 98
 NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
 protein S16 protein - upland cotton
 >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
 [Gossypium hirsutum]

Seq. No. 234395
 Seq. ID LIB3272-034-P1-K1-E4
 Method BLASTX
 NCBI GI g1350944
 BLAST score 367
 E value 3.0e-35
 Match length 76
 % identity 96
 NCBI Description 40S RIBOSOMAL PROTEIN S17

Seq. No. 234396
 Seq. ID LIB3272-034-P1-K1-E6
 Method BLASTX
 NCBI GI g3122673
 BLAST score 412
 E value 2.0e-40
 Match length 112
 % identity 75
 NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447
 (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 234397
 Seq. ID LIB3272-034-P1-K1-E7
 Method BLASTX
 NCBI GI g543867
 BLAST score 369
 E value 2.0e-35
 Match length 104
 % identity 78
 NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
 >gi_1076684_pir_A47493 H+-transporting ATP synthase (EC
 3.6.1.34) gamma chain precursor - sweet potato
 >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gamma subunit
 [Ipomoea batatas]

Seq. No. 234398
 Seq. ID LIB3272-034-P1-K1-E8
 Method BLASTX
 NCBI GI g1332579
 BLAST score 580
 E value 4.0e-60
 Match length 117
 % identity 10
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 234399
 Seq. ID LIB3272-034-P1-K1-E9
 Method BLASTX
 NCBI GI g4220477
 BLAST score 279
 E value 7.0e-25
 Match length 114
 % identity 56
 NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 234400
 Seq. ID LIB3272-034-P1-K1-F10
 Method BLASTX
 NCBI GI g2583134
 BLAST score 243
 E value 1.0e-20
 Match length 123
 % identity 46
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis
 thaliana]

Seq. No. 234401

BLAST score 158
 E value 5.0e-11
 Match length 45
 % identity 71
 NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 234407
 Seq. ID LIB3272-034-P1-K1-F7
 Method BLASTX
 NCBI GI g3643609
 BLAST score 382
 E value 6.0e-37
 Match length 124
 % identity 63
 NCBI Description (AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No. 234408
 Seq. ID LIB3272-034-P1-K1-F8
 Method BLASTX
 NCBI GI g3928095
 BLAST score 171
 E value 3.0e-12
 Match length 109
 % identity 38
 NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No. 234409
 Seq. ID LIB3272-034-P1-K1-G10
 Method BLASTX
 NCBI GI g3212869
 BLAST score 570
 E value 5.0e-59
 Match length 120
 % identity 87
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 234410
 Seq. ID LIB3272-034-P1-K1-G2
 Method BLASTX
 NCBI GI g3158474
 BLAST score 324
 E value 5.0e-36
 Match length 91
 % identity 89
 NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 234411
 Seq. ID LIB3272-034-P1-K1-G4
 Method BLASTX
 NCBI GI g322750
 BLAST score 615
 E value 3.0e-64
 Match length 120
 % identity 98
 NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco
 >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana

DEBILITAS

Seq. No. 234417
Seq. ID LIB3272-034-P1-K1-H11

Method BLASTX
 NCBI GI g1928981
 BLAST score 394
 E value 1.0e-38
 Match length 90
 % identity 53
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 234418
 Seq. ID LIB3272-034-P1-K1-H2
 Method BLASTX
 NCBI GI g1332579
 BLAST score 665
 E value 4.0e-70
 Match length 134
 % identity 10
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 234419
 Seq. ID LIB3272-034-P1-K1-H5
 Method BLASTX
 NCBI GI g4103324
 BLAST score 529
 E value 4.0e-54
 Match length 111
 % identity 92
 NCBI Description (AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]

Seq. No. 234420
 Seq. ID LIB3272-034-P1-K1-H6
 Method BLASTX
 NCBI GI g475048
 BLAST score 527
 E value 6.0e-54
 Match length 115
 % identity 58
 NCBI Description (X72581) tonoplast intrinsic protein gamma (gamma-TIP) [Arabidopsis thaliana]

Seq. No. 234421
 Seq. ID LIB3272-034-P1-K1-H8
 Method BLASTX
 NCBI GI g585973
 BLAST score 602
 E value 1.0e-62
 Match length 130
 % identity 91
 NCBI Description FRUCTOKINASE >gi_626018_pir_S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283 (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf_2108342A fructokinase [Solanum tuberosum]

Seq. No. 234422
 Seq. ID LIB3272-034-P1-K1-H9
 Method BLASTX

Seq. ID LIB3272-035-P1-K1-A3
 Method BLASTX
 NCBI GI g1709498
 BLAST score 559
 E value 1.0e-57
 Match length 125
 % identity 80
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 234426
 Seq. ID LIB3272-035-P1-K1-A6
 Method BLASTX
 NCBI GI g2078350
 BLAST score 606
 E value 4.0e-63
 Match length 138
 % identity 83
 NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 234427
 Seq. ID LIB3272-035-P1-K1-A8
 Method BLASTX
 NCBI GI g133249
 BLAST score 311
 E value 1.0e-28
 Match length 78
 % identity 45
 NCBI Description CHLOROPLAST 33 KD RIBONUCLEOPROTEIN PRECURSOR
 >gi_100390_pir_S12111 ribonucleoprotein, 33K, precursor -
 common tobacco >gi_20005_emb_CAA37879_ (X53932) 33 kDa
 ribonucleoprotein precursor [Nicotiana tabacum]

Seq. No. 234428
 Seq. ID LIB3272-035-P1-K1-A9
 Method BLASTX
 NCBI GI g3894159
 BLAST score 228
 E value 8.0e-19
 Match length 130
 % identity 38
 NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No. 234429
 Seq. ID LIB3272-035-P1-K1-B1
 Method BLASTX
 NCBI GI g1945611
 BLAST score 301
 E value 2.0e-27
 Match length 134
 % identity 45
 NCBI Description (AB003103) 26S proteasome subunit p55 [Homo sapiens]
 >gi_4506221_ref_NP_002807.1_pPSMD12_ proteasome (prosome,
 macropain) 26S subunit, non-ATPase,

Seq. No. 234430
 Seq. ID LIB3272-035-P1-K1-B10
 Method BLASTX
 NCBI GI g119355
 BLAST score 506
 E value 1.0e-51
 Match length 112
 % identity 88
 NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
 >gi_100869_pir_S16257 phosphopyruvate hydratase (EC
 4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
 [Zea mays]

Seq. No. 234431
 Seq. ID LIB3272-035-P1-K1-B12
 Method BLASTX
 NCBI GI g2462929
 BLAST score 486
 E value 5.0e-49
 Match length 144
 % identity 64
 NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No. 234432
 Seq. ID LIB3272-035-P1-K1-B4
 Method BLASTX
 NCBI GI g133867
 BLAST score 371
 E value 9.0e-36
 Match length 91
 % identity 80
 NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal
 protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
 ribosomal protein S11 [Zea mays]

Seq. No. 234433
 Seq. ID LIB3272-035-P1-K1-C2
 Method BLASTX
 NCBI GI g126770
 BLAST score 705
 E value 1.0e-74
 Match length 134
 % identity 100
 NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir_SYCNMU malate
 synthase (EC 4.1.3.2) - upland cotton
 >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
 [Gossypium hirsutum]

Seq. No. 234434
 Seq. ID LIB3272-035-P1-K1-C3
 Method BLASTX
 NCBI GI g548774
 BLAST score 421
 E value 2.0e-41
 Match length 108
 % identity 76

% identity 49
 NCBI Description CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4)
 >gi_480396_pir_S36806 cytochrome P450 71A2 - eggplant
 >gi_408140_emb_CAA50645 (X71654) P450 hydroxylase [Solanum
 melongena] >gi_441185_dbj_BAA03635_ (D14990) Cytochrome
 P-450EG4 [Solanum melongena]

Seq. No. 234439
 Seq. ID LIB3272-035-P1-K1-D10
 Method BLASTX
 NCBI GI g1173209
 BLAST score 660
 E value 2.0e-69
 Match length 140
 % identity 93

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir_S41193 ribosomal
 protein S16 protein - upland cotton
 >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
 [Gossypium hirsutum]

Seq. No. 234440
 Seq. ID LIB3272-035-P1-K1-D11
 Method BLASTX
 NCBI GI g3158376
 BLAST score 309
 E value 3.0e-28
 Match length 118
 % identity 56
 NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 234441
 Seq. ID LIB3272-035-P1-K1-D12
 Method BLASTX
 NCBI GI g3063470
 BLAST score 547
 E value 3.0e-56
 Match length 100
 % identity 96
 NCBI Description (AC003981) F22013.32 [Arabidopsis thaliana]

Seq. No. 234442
 Seq. ID LIB3272-035-P1-K1-D5
 Method BLASTX
 NCBI GI g4490321
 BLAST score 297
 E value 7.0e-27
 Match length 115
 % identity 54
 NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No. 234443
 Seq. ID LIB3272-035-P1-K1-D7
 Method BLASTX
 NCBI GI g529353
 BLAST score 214
 E value 4.0e-17
 Match length 105

% identity	45
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]
Seq. No.	234444
Seq. ID	LIB3272-035-P1-K1-D8
Method	BLASTX
NCBI GI	g1729971
BLAST score	220
E value	2.0e-18
Match length	109
% identity	51
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_1076745_pir_S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa]
Seq. No.	234445
Seq. ID	LIB3272-035-P1-K1-D9
Method	BLASTX
NCBI GI	g2511594
BLAST score	641
E value	3.0e-67
Match length	139
% identity	86
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.	234446
Seq. ID	LIB3272-035-P1-K1-E11
Method	BLASTX
NCBI GI	g419781
BLAST score	138
E value	1.0e-08
Match length	45
% identity	64
NCBI Description	probable cysteine proteinase precursor (clone CYP-7) - common tobacco >gi_19849_emb_CAA78361_ (Z13959) tobacco pre-pro-cysteine proteinase [Nicotiana tabacum]
Seq. No.	234447
Seq. ID	LIB3272-035-P1-K1-E12
Method	BLASTX
NCBI GI	g3421102
BLAST score	392
E value	3.0e-38
Match length	86
% identity	83
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]
Seq. No.	234448
Seq. ID	LIB3272-035-P1-K1-E2
Method	BLASTX

E value 3.0e-72
 Match length 126
 % identity 99
 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
 hirsutum]

Seq. No. 234474
 Seq. ID LIB3272-036-P1-K1-A12
 Method BLASTX
 NCBI GI g81454
 BLAST score 596
 E value 5.0e-62
 Match length 128
 % identity 91
 NCBI Description photosystem II oxygen-evolving complex protein 1 - spinach
 >gi_224916_prf_1204192A photosystem II protein 33kD
 [Spinacia oleracea]

Seq. No. 234475
 Seq. ID LIB3272-036-P1-K1-A3
 Method BLASTX
 NCBI GI g1709498
 BLAST score 488
 E value 2.0e-49
 Match length 109
 % identity 81
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
 thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
 [Arabidopsis thaliana]

Seq. No. 234476
 Seq. ID LIB3272-036-P1-K1-A4
 Method BLASTX
 NCBI GI g2088652
 BLAST score 383
 E value 2.0e-44
 Match length 119
 % identity 76
 NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog
 [Arabidopsis thaliana] >gi_2351376 (U54561) translation
 initiation factor eIF2 p47 subunit homolog [Arabidopsis
 thaliana]

Seq. No. 234477
 Seq. ID LIB3272-036-P1-K1-A6
 Method BLASTX
 NCBI GI g549063
 BLAST score 365
 E value 5.0e-35
 Match length 92
 % identity 75
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1072464_pir_A38958 IgE-dependent histamine-releasing
 factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
 21kd polypeptide [Oryza sativa]

09664015-101000

Seq. No. 234478
 Seq. ID LIB3272-036-P1-K1-A7
 Method BLASTX
 NCBI GI g3986695
 BLAST score 645
 E value 9.0e-68
 Match length 139
 % identity 93
 NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 234479
 Seq. ID LIB3272-036-P1-K1-A8
 Method BLASTX
 NCBI GI g464986
 BLAST score 493
 E value 7.0e-50
 Match length 92
 % identity 98
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
 >gi_421857_pir_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
 >gi_297884_emb_CAA78714_(Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
 >gi_600391_emb_CAA51201_(X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
 >gi_4455355_emb_CAB36765.1_(AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 234480
 Seq. ID LIB3272-036-P1-K1-B12
 Method BLASTX
 NCBI GI g2146740
 BLAST score 408
 E value 6.0e-40
 Match length 111
 % identity 72
 NCBI Description inner mitochondrial membrane protein - Arabidopsis thaliana
 >gi_603056 (U18126) inner mitochondrial membrane protein [Arabidopsis thaliana]

Seq. No. 234481
 Seq. ID LIB3272-036-P1-K1-B4
 Method BLASTX
 NCBI GI g4191788
 BLAST score 453
 E value 3.0e-45
 Match length 128
 % identity 65
 NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No. 234482
 Seq. ID LIB3272-036-P1-K1-B5
 Method BLASTX
 NCBI GI g3334123

BLAST score 288
 E value 6.0e-26
 Match length 85
 % identity 74
 NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
 >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
 mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787
 (AC002334) mitochondrial F1-ATPase, gamma subunit
 [Arabidopsis thaliana]

Seq. No. 234483
 Seq. ID LIB3272-036-P1-K1-B6
 Method BLASTX
 NCBI GI g1172597
 BLAST score 229
 E value 4.0e-19
 Match length 47
 % identity 94
 NCBI Description WOUND-INDUCED BASIC PROTEIN >gi_81888_pir_JS0731
 wound-inducible basic protein - kidney bean >gi_169365
 (L00625) basic protein [Phaseolus vulgaris]
 >gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein
 [Phaseolus vulgaris]

Seq. No. 234484
 Seq. ID LIB3272-036-P1-K1-B7
 Method BLASTX
 NCBI GI g4510363
 BLAST score 523
 E value 2.0e-53
 Match length 110
 % identity 89
 NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
 thaliana]

Seq. No. 234485
 Seq. ID LIB3272-036-P1-K1-B9
 Method BLASTX
 NCBI GI g2129871
 BLAST score 278
 E value 1.0e-24
 Match length 89
 % identity 62
 NCBI Description proline-rich protein, 14K - kidney bean >gi_1420885
 (U34333) proline-rich 14 kDa protein [Phaseolus vulgaris]

Seq. No. 234486
 Seq. ID LIB3272-036-P1-K1-C10
 Method BLASTX
 NCBI GI g3986695
 BLAST score 616
 E value 2.0e-64
 Match length 135
 % identity 91
 NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 234487

09584016-101000

Method BLASTX
NCBI GI g1353059
BLAST score 179
E value 4.0e-13
Match length 124
% identity 32
NCBI Description HYPOTHETICAL 27.4 KD PROTEIN IN MER2-BNA1 INTERGENIC REGION
>gi_1077874_pir_S57042 hypothetical protein YJR024c -
yeast (Saccharomyces cerevisiae) >gi_1015663_emb_CAA89549_
(Z49524) ORF YJR024c [Saccharomyces cerevisiae]
>gi_1129160_emb_CAA60719_ (X87297) J1545 [Saccharomyces
cerevisiae]

Seq. No. 234499
Seq. ID LIB3272-036-P1-K1-D8
Method BLASTX
NCBI GI g4115377
BLAST score 344
E value 2.0e-32
Match length 113
% identity 52
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 234500
Seq. ID LIB3272-036-P1-K1-D9
Method BLASTX
NCBI GI g3128231
BLAST score 315
E value 5.0e-29
Match length 132
% identity 11
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
>gi_3337370 (AC004481) hypothetical protein [Arabidopsis
thaliana]

Seq. No. 234501
Seq. ID LIB3272-036-P1-K1-E1
Method BLASTX
NCBI GI g2388585
BLAST score 208
E value 2.0e-16
Match length 68
% identity 65
NCBI Description (AC000098) Similar to Caenorhabditis unknown protein
T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No. 234502
Seq. ID LIB3272-036-P1-K1-E10
Method BLASTX
NCBI GI g1173218
BLAST score 585
E value 1.0e-60
Match length 115
% identity 98
NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	234503
Seq. ID	LIB3272-036-P1-K1-E2
Method	BLASTX
NCBI GI	g3763932
BLAST score	219
E value	9.0e-18
Match length	68
% identity	62
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]
Seq. No.	234504
Seq. ID	LIB3272-036-P1-K1-E4
Method	BLASTX
NCBI GI	g2651310
BLAST score	239
E value	4.0e-20
Match length	129
% identity	35
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]
Seq. No.	234505
Seq. ID	LIB3272-036-P1-K1-E6
Method	BLASTX
NCBI GI	g4204313
BLAST score	160
E value	7.0e-11
Match length	79
% identity	42
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	234506
Seq. ID	LIB3272-036-P1-K1-E7
Method	BLASTX
NCBI GI	g461498
BLAST score	536
E value	6.0e-55
Match length	134
% identity	75
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]
Seq. No.	234507
Seq. ID	LIB3272-036-P1-K1-E8
Method	BLASTX
NCBI GI	g3386621
BLAST score	507
E value	1.0e-51
Match length	118
% identity	81
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]


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NCBI GI          g266972
BLAST score      204
E value          5.0e-16
Match length     54
% identity       65
NCBI Description  40S RIBOSOMAL PROTEIN S29 >gi_631884_pir_S30298 ribosomal
                  protein S29 - rat >gi_1362934_pir_S55919 ribosomal protein
                  S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal
                  protein S29 [Rattus norvegicus] >gi_550027 (U14973)
                  ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610)
                  homologous to antisense sequence of krev-1, anti oncogene
                  [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein
                  [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29
                  [Bos taurus] >gi_1096945_prf_2113200H ribosomal protein
                  S29 [Homo sapiens] >gi_4506717_ref_NP_001023.1_pRPS29_
                  ribosomal protein S29

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Seq. No.          234519
Seq. ID           LIB3272-036-P1-K1-G3
Method            BLASTX
NCBI GI           g4249382
BLAST score       457
E value           9.0e-46
Match length      121
% identity        69
NCBI Description   (AC005966) Strong similarity to gi_3337350 F13P17.3
                   putative permease from Arabidopsis thaliana BAC
                   qb AC004481. [Arabidopsis thaliana]
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Seq. No.          234520
Seq. ID           LIB3272-036-P1-K1-G4
Method            BLASTX
NCBI GI           g1703108
BLAST score       718
E value           3.0e-76
Match length      133
% identity        100
NCBI Description   ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis
                  thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis
                  thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                  thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                  thaliana]
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Seq. No.	234521
Seq. ID	LIB3272-036-P1-K1-G5
Method	BLASTX
NCBI GI	g2160166
BLAST score	376
E value	3.0e-36
Match length	136
% identity	56
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	234522
Seq. ID	LIB3272-036-P1-K1-G6
Method	BLASTX
NCBI GI	q543867

Seq. No. 234536
 Seq. ID LIB3272-037-P1-K1-B1
 Method BLASTX
 NCBI GI g3063396
 BLAST score 527
 E value 7.0e-54
 Match length 117
 % identity 85
 NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 234537
 Seq. ID LIB3272-037-P1-K1-B10
 Method BLASTX
 NCBI GI g3450889
 BLAST score 358
 E value 3.0e-34
 Match length 102
 % identity 74
 NCBI Description (AF083890) 19S proteasome subunit 9 [Arabidopsis thaliana]

Seq. No. 234538
 Seq. ID LIB3272-037-P1-K1-B12
 Method BLASTX
 NCBI GI g462195
 BLAST score 442
 E value 6.0e-44
 Match length 92
 % identity 93
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
 >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 234539
 Seq. ID LIB3272-037-P1-K1-B2
 Method BLASTX
 NCBI GI g730456
 BLAST score 305
 E value 1.0e-41
 Match length 118
 % identity 69
 NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 234540
 Seq. ID LIB3272-037-P1-K1-B3
 Method BLASTX
 NCBI GI g266945
 BLAST score 558
 E value 2.0e-57
 Match length 127
 % identity 87
 NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
 >gi_100065_pir_S19978 ribosomal protein L9 - garden pea
 >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
 >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9 [Pisum sativum]


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Seq. No.      234541
Seq. ID      LIB3272-037-P1-K1-B4
Method       BLASTX
NCBI GI      g1586940
BLAST score   358
E value      4.0e-34
Match length  100
% identity    67
NCBI Description Ser/Thr kinase [Lycopersicon esculentum]
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Seq. No.      234542
Seq. ID      LIB3272-037-P1-K1-B7
Method       BLASTX
NCBI GI      g120669
BLAST score   428
E value      3.0e-42
Match length  94
% identity    86
NCBI Description  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_(X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]
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Seq. No.      234543
Seq. ID      LIB3272-037-P1-K1-B9
Method       BLASTX
NCBI GI      g2507421
BLAST score   519
E value      6.0e-53
Match length  109
% identity   91
NCBI Description  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
                (U81042) translation initiation factor [Arabidopsis
                thaliana] >gi_4490709_emb_CAB38843.1 (AL035680)
                translation initiation factor [Arabidopsis thaliana]
```

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Seq. No.      234544
Seq. ID       LIB3272-037-P1-K1-C1
Method        BLASTX
NCBI GI       g3668089
BLAST score   234
E value       2.0e-19
Match length  83
% identity    51
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
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Seq. No.      234545
Seq. ID      LIB3272-037-P1-K1-C10
Method       BLASTX
NCBI GI      g3851636
BLAST score   424
E value      6.0e-42
Match length  100
% identity    80
NCBI Description (AF098519) unknown [Avicennia marina] >gi 4128206
```


0994016 10100

Seq. ID LIB3272-037-P1-K1-C9
 Method BLASTX
 NCBI GI g3249084
 BLAST score 266
 E value 2.0e-23
 Match length 103
 % identity 18
 NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from *Mus musculus*. ESTs gb_AA712687 and gb_Z37223 come from this gene [*Arabidopsis thaliana*]

Seq. No. 234552
 Seq. ID LIB3272-037-P1-K1-D11
 Method BLASTX
 NCBI GI g629670
 BLAST score 288
 E value 7.0e-26
 Match length 95
 % identity 61
 NCBI Description hypothetical protein - tomato

Seq. No. 234553
 Seq. ID LIB3272-037-P1-K1-D2
 Method BLASTX
 NCBI GI g231504
 BLAST score 668
 E value 2.0e-70
 Match length 137
 % identity 96
 NCBI Description ACTIN 100 >gi_100420_pir_S20092 actin - potato (fragment) >gi_1345579_emb_CAA39276_ (X55746) actin [*Solanum tuberosum*]

Seq. No. 234554
 Seq. ID LIB3272-037-P1-K1-D6
 Method BLASTX
 NCBI GI g3281853
 BLAST score 162
 E value 4.0e-11
 Match length 33
 % identity 94
 NCBI Description (AL031004) putative protein [*Arabidopsis thaliana*]

Seq. No. 234555
 Seq. ID LIB3272-037-P1-K1-D7
 Method BLASTX
 NCBI GI g3023847
 BLAST score 329
 E value 7.0e-31
 Match length 83
 % identity 80
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [*Medicago sativa*]

Seq. No. 234556
 Seq. ID LIB3272-037-P1-K1-D9


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BLAST score      2464
E value          4.0e-49
Match length     107
% identity       98
NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone
H3.3-like protein - Arabidopsis thaliana
>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
(U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
[Medicago sativa] >gi_488577 (U09465) histone H3.2
[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)
histone H3 variant H3.3 [Lycopersicon esculentum]
>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
(AL035708) Histone H3 [Arabidopsis thaliana]

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Seq. No.      234592
Seq. ID       L1B3272-038-P1-K1-A8
Method        BLASTX
NCBI GI       g1173209
BLAST score    227
E value        2.0e-19
Match length   48
% identity     92
NCBI Description  40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
protein S16 protein - upland cotton
>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
[Gossypium hirsutum]
```

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Seq. No.      234594
Seq. ID       LIB3272-038-P1-K1-B5
Method        BLASTX
NCBI GI       g4406768
BLAST score    240
E value        3.0e-20
Match length   103
```


Seq. No. 234600
 Seq. ID LIB3272-038-P1-K1-C4
 Method BLASTX
 NCBI GI g3033400
 BLAST score 522
 E value 3.0e-53
 Match length 123
 % identity 79
 NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 234601
 Seq. ID LIB3272-038-P1-K1-C7
 Method BLASTX
 NCBI GI g3510256
 BLAST score 187
 E value 5.0e-14
 Match length 101
 % identity 44
 NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 234602
 Seq. ID LIB3272-038-P1-K1-C9
 Method BLASTX
 NCBI GI g1709498
 BLAST score 341
 E value 3.0e-32
 Match length 84
 % identity 75
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis thaliana
 >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No. 234603
 Seq. ID LIB3272-038-P1-K1-D10
 Method BLASTX
 NCBI GI g3337366
 BLAST score 368
 E value 3.0e-35
 Match length 135
 % identity 29
 NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]

Seq. No. 234604
 Seq. ID LIB3272-038-P1-K1-D11
 Method BLASTX
 NCBI GI g2500399
 BLAST score 475
 E value 8.0e-48
 Match length 109
 % identity 90
 NCBI Description 40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098)
 ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls, embryos, Peptide, 253 aa] [Ambystoma mexicanum]

E value 9.0e-58
 Match length 121
 % identity 90
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir_JQ1187
 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
 thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
 [Arabidopsis thaliana]

Seq. No. 234611
 Seq. ID LIB3272-038-P1-K1-E2
 Method BLASTX
 NCBI GI g125606
 BLAST score 457
 E value 9.0e-46
 Match length 99
 % identity 88
 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248
 pyruvate kinase (EC 2.7.1.40) - potato
 >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
 tuberosum]

Seq. No. 234612
 Seq. ID LIB3272-038-P1-K1-E4
 Method BLASTX
 NCBI GI g2388575
 BLAST score 211
 E value 8.0e-17
 Match length 116
 % identity 39
 NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 234613
 Seq. ID LIB3272-038-P1-K1-E5
 Method BLASTX
 NCBI GI g136636
 BLAST score 560
 E value 9.0e-58
 Match length 106
 % identity 96
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
 LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
 >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 -
 Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin
 Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK
 Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
 >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
 thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme
 [Arabidopsis thaliana]

Seq. No. 234614
 Seq. ID LIB3272-038-P1-K1-E9
 Method BLASTX
 NCBI GI g117988
 BLAST score 265
 E value 3.0e-23
 Match length 74

Seq. ID LIB3272-038-P1-K1-F7
 Method BLASTX
 NCBI GI g4406780
 BLAST score 414
 E value 1.0e-40
 Match length 103
 % identity 75
 NCBI Description (AC006532) putative multispanning membrane protein
 [Arabidopsis thaliana]

Seq. No. 234621
 Seq. ID LIB3272-038-P1-K1-G1
 Method BLASTX
 NCBI GI g2827552
 BLAST score 459
 E value 6.0e-46
 Match length 128
 % identity 51
 NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 234622
 Seq. ID LIB3272-038-P1-K1-G11
 Method BLASTX
 NCBI GI g119350
 BLAST score 387
 E value 1.0e-37
 Match length 86
 % identity 90
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir_JQ1187
 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
 thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
 [Arabidopsis thaliana]

Seq. No. 234623
 Seq. ID LIB3272-038-P1-K1-G12
 Method BLASTX
 NCBI GI g1922278
 BLAST score 227
 E value 3.0e-19
 Match length 48
 % identity 85
 NCBI Description (Z86091) TCTP protein [Fragaria x ananassa]

Seq. No. 234624
 Seq. ID LIB3272-038-P1-K1-G2
 Method BLASTX
 NCBI GI g924951
 BLAST score 156
 E value 2.0e-10
 Match length 47
 % identity 62
 NCBI Description (U30324) class I chitinase [Theobroma cacao]

Seq. No. 234625
 Seq. ID LIB3272-038-P1-K1-G3
 Method BLASTX

NCBI Description (M92094) aspartate aminotransferase P1 [Lupinus angustifolius]

Seq. No. 234635
 Seq. ID LIB3272-039-P1-K1-A7
 Method BLASTX
 NCBI GI g3068713
 BLAST score 137
 E value 9.0e-09
 Match length 36
 % identity 83

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 234636
 Seq. ID LIB3272-039-P1-K1-B11
 Method BLASTX
 NCBI GI g1709498
 BLAST score 496
 E value 2.0e-50
 Match length 122
 % identity 75

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No. 234637
 Seq. ID LIB3272-039-P1-K1-B12
 Method BLASTX
 NCBI GI g1086252
 BLAST score 421
 E value 1.0e-41
 Match length 114
 % identity 68

NCBI Description sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No. 234638
 Seq. ID LIB3272-039-P1-K1-B3
 Method BLASTX
 NCBI GI g2129772
 BLAST score 326
 E value 2.0e-30
 Match length 96
 % identity 68

NCBI Description xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No. 234639
 Seq. ID LIB3272-039-P1-K1-B4
 Method BLASTX
 NCBI GI g1947137
 BLAST score 342
 E value 3.0e-32

Match length	123
% identity	50
NCBI Description	(AF000264) similar to the ATP-binding transport protein family (ABC transporters). [Caenorhabditis elegans]
Seq. No.	234640
Seq. ID	LIB3272-039-P1-K1-B5
Method	BLASTX
NCBI GI	g1351411
BLAST score	382
E value	6.0e-37
Match length	98
% identity	72
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B) >gi_1076553_pir_S49175 cysteine proteinase precursor - spring vetch >gi_2129906_pir_S68984 cysteine proteinase precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899) cysteine proteinase [Vicia sativa]
Seq. No.	234641
Seq. ID	LIB3272-039-P1-K1-B6
Method	BLASTX
NCBI GI	g2791834
BLAST score	399
E value	1.0e-51
Match length	109
% identity	95
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.	234642
Seq. ID	LIB3272-039-P1-K1-B9
Method	BLASTX
NCBI GI	g1370194
BLAST score	447
E value	8.0e-45
Match length	92
% identity	97
NCBI Description	(Z73946) RAB8C [Lotus japonicus]
Seq. No.	234643
Seq. ID	LIB3272-039-P1-K1-C1
Method	BLASTX
NCBI GI	g3980393
BLAST score	369
E value	2.0e-35
Match length	102
% identity	68
NCBI Description	(AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
Seq. No.	234644
Seq. ID	LIB3272-039-P1-K1-C12
Method	BLASTX
NCBI GI	g2984709
BLAST score	416
E value	6.0e-41
Match length	83

% identity	93
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.	234645
Seq. ID	LIB3272-039-P1-K1-C3
Method	BLASTX
NCBI GI	g117188
BLAST score	261
E value	6.0e-23
Match length	99
% identity	47
NCBI Description	CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2) >gi_81423_pir__A35867 cytochrome P450 71A1 - avocado
Seq. No.	234646
Seq. ID	LIB3272-039-P1-K1-C6
Method	BLASTX
NCBI GI	g167367
BLAST score	571
E value	3.0e-59
Match length	106
% identity	98
NCBI Description	(L08199) peroxidase [Gossypium hirsutum]
Seq. No.	234647
Seq. ID	LIB3272-039-P1-K1-C7
Method	BLASTX
NCBI GI	g2262159
BLAST score	399
E value	4.0e-39
Match length	93
% identity	78
NCBI Description	(AC002329) predicted protein similar to S.pombe protein C5H10.03 [Arabidopsis thaliana]
Seq. No.	234648
Seq. ID	LIB3272-039-P1-K1-C8
Method	BLASTX
NCBI GI	g2129944
BLAST score	333
E value	9.0e-32
Match length	72
% identity	85
NCBI Description	RNA-binding protein RZ-1 - wood tobacco >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]
Seq. No.	234649
Seq. ID	LIB3272-039-P1-K1-D10
Method	BLASTX
NCBI GI	g2738949
BLAST score	291
E value	2.0e-26
Match length	104
% identity	57
NCBI Description	(AF022213) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 234650
 Seq. ID LIB3272-039-P1-K1-D11
 Method BLASTX
 NCBI GI g4206789
 BLAST score 251
 E value 1.0e-21
 Match length 66
 % identity 71
 NCBI Description (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No. 234651
 Seq. ID LIB3272-039-P1-K1-D12
 Method BLASTX
 NCBI GI g4105772
 BLAST score 425
 E value 5.0e-42
 Match length 111
 % identity 43
 NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 234652
 Seq. ID LIB3272-039-P1-K1-D2
 Method BLASTX
 NCBI GI g133249
 BLAST score 160
 E value 5.0e-11
 Match length 47
 % identity 38
 NCBI Description CHLOROPLAST 33 KD RIBONUCLEOPROTEIN PRECURSOR
 >gi_100390_pir_S12111 ribonucleoprotein, 33K, precursor -
 common tobacco >gi_20005_emb_CAA37879_ (X53932) 33 kDa
 ribonucleoprotein precursor [Nicotiana tabacum]

Seq. No. 234653
 Seq. ID LIB3272-039-P1-K1-D3
 Method BLASTX
 NCBI GI g3367578
 BLAST score 298
 E value 3.0e-27
 Match length 84
 % identity 68
 NCBI Description (AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 234654
 Seq. ID LIB3272-039-P1-K1-D4
 Method BLASTX
 NCBI GI g3297827
 BLAST score 253
 E value 8.0e-22
 Match length 85
 % identity 65
 NCBI Description (AL031032) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	234660
Seq. ID	LIB3272-039-P1-K1-E10
Method	BLASTX
NCBI GI	g4098128
BLAST score	467
E value	5.0e-47
Match length	102
% identity	89
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.	234661
Seq. ID	LIB3272-039-P1-K1-E11
Method	BLASTX
NCBI GI	g481236
BLAST score	299
E value	4.0e-27
Match length	72
% identity	82
NCBI Description	hypothetical protein - Madagascar periwinkle >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide [Catharanthus roseus]
Seq. No.	234662
Seq. ID	LIB3272-039-P1-K1-E3
Method	BLASTX
NCBI GI	g115492
BLAST score	558
E value	1.0e-57
Match length	110
% identity	54
NCBI Description	CALMODULIN-RELATED PROTEIN >gi_169205 (M80831) calmodulin-related protein [Petunia hybrida]
Seq. No.	234663
Seq. ID	LIB3272-039-P1-K1-E5
Method	BLASTX
NCBI GI	g4572679
BLAST score	182
E value	8.0e-14
Match length	45
% identity	73
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]
Seq. No.	234664
Seq. ID	LIB3272-039-P1-K1-E6
Method	BLASTX
NCBI GI	g508304
BLAST score	208
E value	1.0e-16
Match length	50
% identity	80
NCBI Description	(L22305) corC [Medicago sativa]
Seq. No.	234665
Seq. ID	LIB3272-039-P1-K1-E7

Method BLASTX
 NCBI GI g730463
 BLAST score 322
 E value 7.0e-30
 Match length 105
 % identity 59
 NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
 >gi_630323_pir_S44069 ribosomal protein L35a.e.c15 - yeast
 (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
 protein L37 [Saccharomyces cerevisiae]
 >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
 [Saccharomyces cerevisiae]

Seq. No. 234671
 Seq. ID LIB3272-039-P1-K1-F2
 Method BLASTX
 NCBI GI g548852
 BLAST score 301
 E value 1.0e-27
 Match length 71
 % identity 80
 NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal
 protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
 subunit ribosomal protein [Oryza sativa]

Seq. No. 234672
 Seq. ID LIB3272-039-P1-K1-F3
 Method BLASTX
 NCBI GI g2979544
 BLAST score 162
 E value 2.0e-11
 Match length 92
 % identity 40
 NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No. 234673
 Seq. ID LIB3272-039-P1-K1-F9
 Method BLASTX
 NCBI GI g120669
 BLAST score 445
 E value 1.0e-44
 Match length 93
 % identity 88
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
 dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
 >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 234674
 Seq. ID LIB3272-039-P1-K1-G3
 Method BLASTX
 NCBI GI g549063
 BLAST score 316
 E value 3.0e-29
 Match length 81
 % identity 74

Method BLASTX
 NCBI GI g1928981
 BLAST score 525
 E value 1.0e-53
 Match length 117
 % identity 91
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 234705
 Seq. ID LIB3272-040-P1-K1-E1
 Method BLASTX
 NCBI GI g3860277
 BLAST score 397
 E value 5.0e-42
 Match length 129
 % identity 74
 NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 234706
 Seq. ID LIB3272-040-P1-K1-E10
 Method BLASTX
 NCBI GI g4102723
 BLAST score 567
 E value 1.0e-58
 Match length 120
 % identity 70
 NCBI Description (AF015784) TATA-box binding protein [Phaseolus vulgaris]

Seq. No. 234707
 Seq. ID LIB3272-040-P1-K1-E12
 Method BLASTX
 NCBI GI g1173043
 BLAST score 318
 E value 2.0e-29
 Match length 68
 % identity 91
 NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi_479441_pir_S33899 ribosomal protein L38 - tomato (cv. MoneyMaker)
 >gi_313027_emb_CAA49599_ (X69979) ribosomal protein L38 [Lycopersicon esculentum]

Seq. No. 234708
 Seq. ID LIB3272-040-P1-K1-E2
 Method BLASTX
 NCBI GI g3063454
 BLAST score 140
 E value 1.0e-08
 Match length 101
 % identity 37
 NCBI Description (AC003981) F22013.16 [Arabidopsis thaliana]

Seq. No. 234709
 Seq. ID LIB3272-040-P1-K1-E4
 Method BLASTX


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E value          5.0e-27
Match length     111
% identity       56
NCBI Description gene 1-Sc3 protein - European white birch
>gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
>gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
pendula]
```

```
Seq. No.      234740
Seq. ID       LIB3272-041-P1-K1-F2
Method        BLASTX
NCBI GI       g3023841
BLAST score    221
E value       6.0e-18
Match length   54
% identity     76
NCBI Description  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT
                >gi_1695179_emb_CAA70704_ (Y09513) G protein beta subunit
                [Nicotiana glauca]
```

```
Seq. No.      234741
Seq. ID      LIB3272-041-P1-K1-F4
Method       BLASTX
NCBI GI      g4371282
BLAST score   521
E value      3.0e-53
Match length  117
% identity   85
NCBI Description (AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]
```

```
Seq. No.          234742
Seq. ID           LIB3272-041-P1-K1-F6
Method            BLASTX
NCBI GI           g232031
BLAST score       219
E value           8.0e-18
Match length      67
% identity        60
NCBI Description   ELONGATION*FACTOR 1 BETA' >gi_322851_pir_S29224
                  translation elongation factor eEF-1 beta' chain - rice
                  >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                  [Oryza sativa]
```

Seq. No.	234743
Seq. ID	LIB3272-041-P1-K1-F8
Method	BLASTX
NCBI GI	g3023841
BLAST score	162
E value	4.0e-11
Match length	54
% identity	59
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi_1695179_emb_CAA70704_ (Y09513) G protein beta subunit [Nicotiana glauca]

Seq. No. 234744

Seq. ID	LIB3272-041-P1-K1-F9
Method	BLASTX
NCBI GI	g2924520
BLAST score	547
E value	3.0e-56
Match length	123
% identity	86
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]
Seq. No.	234745
Seq. ID	LIB3272-041-P1-K1-G11
Method	BLASTX
NCBI GI	g2961085
BLAST score	110
E value	3.0e-09
Match length	96
% identity	44
NCBI Description	(AF037228) transcription factor [Arabidopsis thaliana]
Seq. No.	234746
Seq. ID	LIB3272-041-P1-K1-G2
Method	BLASTX
NCBI GI	g3608140
BLAST score	159
E value	1.0e-10
Match length	87
% identity	41
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.	234747
Seq. ID	LIB3272-041-P1-K1-G3
Method	BLASTX
NCBI GI	g3608485
BLAST score	502
E value	5.0e-51
Match length	101
% identity	93
NCBI Description	(AF088915) proteasome beta subunit [Petunia x hybrida]
Seq. No.	234748
Seq. ID	LIB3272-041-P1-K1-H1
Method	BLASTX
NCBI GI	g3024583
BLAST score	184
E value	7.0e-14
Match length	96
% identity	48
NCBI Description	RT14 PROTEIN HOMOLOG >gi_2347196 (AC002338) RT14 protein isolog [Arabidopsis thaliana]
Seq. No.	234749
Seq. ID	LIB3272-041-P1-K1-H2
Method	BLASTX
NCBI GI	g2984709
BLAST score	385
E value	3.0e-37

Match length 80
 % identity 90
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
 Seq. No. 234750
 Seq. ID LIB3272-041-P1-K1-H3
 Method BLASTX
 NCBI GI g3023858
 BLAST score 431
 E value 1.0e-42
 Match length 93
 % identity 86
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No. 234751
 Seq. ID LIB3272-041-P1-K1-H7
 Method BLASTX
 NCBI GI g4115949
 BLAST score 195
 E value 3.0e-15
 Match length 63
 % identity 65
 NCBI Description (AF118223) contains similarity to adenosine deaminases [Arabidopsis thaliana]

Seq. No. 234752
 Seq. ID LIB3272-041-P1-K1-H8
 Method BLASTX
 NCBI GI g1408471
 BLAST score 447
 E value 2.0e-44
 Match length 102
 % identity 78
 NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No. 234753
 Seq. ID LIB3272-042-P1-K1-A11
 Method BLASTX
 NCBI GI g2702376
 BLAST score 219
 E value 9.0e-18
 Match length 89
 % identity 46
 NCBI Description (AF038605) Similar to acyl-CoA dehydrogenase; coded for by C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded for by C. elegans cDNA yk158e10.3; coded for by C. elegans cDNA yk427... >gi_4455127_gb_AAD21088_ (AF127558) isovaleryl-CoA dehydrogenase precursor [Caenorhabditis elegans]

Seq. No. 234754
 Seq. ID LIB3272-042-P1-K1-A12

0908016 1000

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Seq. No.      234776
Seq. ID      LIB3272-042-P1-K1-D1
Method       BLASTX
NCBI GI      g70644
BLAST score   611
E value      1.0e-63
Match length  126
% identity    19
NCBI Description  ubiquitin precursor - common sunflower (fragment)
```

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Seq. No.      234778
Seq. ID       LIB3272-042-P1-K1-D12
Method        BLASTX
NCBI GI       g4539390
BLAST score   511
E value       5.0e-52
Match length  112
% identity    88
NCBI Description (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
               [Arabidopsis thaliana]
```

Seq. No.	234780
Seq. ID	LIB3272-042-P1-K1-D5

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 234790
 Seq. ID LIB3272-042-P1-K1-F2
 Method BLASTX
 NCBI GI g3738327
 BLAST score 352
 E value 2.0e-33
 Match length 141
 % identity 50
 NCBI Description (AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 234791
 Seq. ID LIB3272-042-P1-K1-F4
 Method BLASTX
 NCBI GI g487046
 BLAST score 227
 E value 1.0e-18
 Match length 103
 % identity 46
 NCBI Description photosystem I chain II precursor - wood tobacco
 >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
 [Nicotiana sylvestris]

Seq. No. 234792
 Seq. ID LIB3272-042-P1-K1-F5
 Method BLASTX
 NCBI GI g266579
 BLAST score 237
 E value 5.0e-20
 Match length 75
 % identity 61
 NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_169713 (L02306)
 metallothionein [Ricinus communis]

Seq. No. 234793
 Seq. ID LIB3272-042-P1-K1-F7
 Method BLASTX
 NCBI GI g170507
 BLAST score 130
 E value 6.0e-14
 Match length 70
 % identity 59
 NCBI Description (M59251) ORF [Lycopersicon esculentum] >gi_1172167 (U44386)
 heat shock protein [Solanum lycopersicum]

Seq. No. 234794
 Seq. ID LIB3272-042-P1-K1-G1
 Method BLASTX
 NCBI GI g3319882
 BLAST score 716
 E value 5.0e-76
 Match length 141
 % identity 96
 NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No. 234805
 Seq. ID LIB3272-043-P1-K1-A12
 Method BLASTX
 NCBI GI g1332579
 BLAST score 458
 E value 5.0e-55
 Match length 117
 % identity 10
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 234806
 Seq. ID LIB3272-043-P1-K1-A4
 Method BLASTX
 NCBI GI g3603456
 BLAST score 442
 E value 5.0e-44
 Match length 99
 % identity 28
 NCBI Description (AF088848) polyubiquitin [Capsicum chinense]

Seq. No. 234807
 Seq. ID LIB3272-043-P1-K1-A9
 Method BLASTX
 NCBI GI g585165
 BLAST score 168
 E value 8.0e-13
 Match length 64
 % identity 61
 NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi_2129985_pir_S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]

Seq. No. 234808
 Seq. ID LIB3272-043-P1-K1-B10
 Method BLASTX
 NCBI GI g586339
 BLAST score 207
 E value 2.0e-16
 Match length 71
 % identity 54
 NCBI Description PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir_S46098 probable AMP-binding protein - yeast (Saccharomyces cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c [Saccharomyces cerevisiae]

Seq. No. 234809
 Seq. ID LIB3272-043-P1-K1-B12
 Method BLASTX
 NCBI GI g3043428
 BLAST score 435
 E value 4.0e-43
 Match length 93
 % identity 87
 NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. ID LIB3272-043-P1-K1-E7
 Method BLASTX
 NCBI GI g1170747
 BLAST score 309
 E value 2.0e-28
 Match length 74
 % identity 82
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
 (M88324) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167347 (M37697) Lea5-A late
 embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 234832
 Seq. ID LIB3272-043-P1-K1-E8
 Method BLASTX
 NCBI GI g508304
 BLAST score 278
 E value 1.0e-24
 Match length 67
 % identity 78
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 234833
 Seq. ID LIB3272-043-P1-K1-E9
 Method BLASTX
 NCBI GI g2160166
 BLAST score 304
 E value 9.0e-28
 Match length 132
 % identity 48
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 234834
 Seq. ID LIB3272-043-P1-K1-F1
 Method BLASTX
 NCBI GI g3851001
 BLAST score 411
 E value 2.0e-40
 Match length 111
 % identity 75
 NCBI Description (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2
 [Zea mays]

Seq. No. 234835
 Seq. ID LIB3272-043-P1-K1-F11
 Method BLASTX
 NCBI GI g3450889
 BLAST score 271
 E value 5.0e-24
 Match length 81
 % identity 70
 NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 234836
 Seq. ID LIB3272-043-P1-K1-F12
 Method BLASTX
 NCBI GI g4455364

Match length	103
% identity	78
NCBI Description	(L37790) cationic peroxidase [Stylosanthes humilis]
Seq. No.	234842
Seq. ID	LIB3272-043-P1-K1-G2
Method	BLASTX
NCBI GI	g1173218
BLAST score	177
E value	4.0e-13
Match length	86
% identity	49
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.	234843
Seq. ID	LIB3272-043-P1-K1-G3
Method	BLASTX
NCBI GI	g1220196
BLAST score	476
E value	5.0e-48
Match length	97
% identity	94
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.	234844
Seq. ID	LIB3272-043-P1-K1-G4
Method	BLASTX
NCBI GI	g3023847
BLAST score	169
E value	2.0e-12
Match length	42
% identity	76
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]
Seq. No.	234845
Seq. ID	LIB3272-043-P1-K1-G6
Method	BLASTX
NCBI GI	g548852
BLAST score	277
E value	1.0e-24
Match length	82
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S subunit ribosomal protein [Oryza sativa]
Seq. No.	234846
Seq. ID	LIB3272-043-P1-K1-G7
Method	BLASTX
NCBI GI	g3868758
BLAST score	344
E value	1.0e-32
Match length	85

Seq. No.	234852
Seq. ID	LIB3272-044-P1-K1-A1
Method	BLASTX
NCBI GI	g2160166
BLAST score	207
E value	1.0e-16
Match length	105
% identity	51
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.	234853
Seq. ID	LIB3272-044-P1-K1-A10
Method	BLASTX
NCBI GI	g1107526
BLAST score	348
E value	6.0e-33
Match length	100
% identity	66
NCBI Description	(X87931) SIEP1L protein [Beta vulgaris]
Seq. No.	234854
Seq. ID	LIB3272-044-P1-K1-A3
Method	BLASTX
NCBI GI	g2129753
BLAST score	201
E value	1.0e-15
Match length	55
% identity	75
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]
Seq. No.	234855
Seq. ID	LIB3272-044-P1-K1-A5
Method	BLASTX
NCBI GI	g1702983
BLAST score	356
E value	7.0e-34
Match length	111
% identity	59
NCBI Description	AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir_S11850 hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034_ (L44142) auxin-repressed protein [Fragaria ananassa]
Seq. No.	234856
Seq. ID	LIB3272-044-P1-K1-A6
Method	BLASTX
NCBI GI	g1419088
BLAST score	686
E value	1.0e-72
Match length	133
% identity	96
NCBI Description	(Z71395) calreticulin [Nicotiana plumbaginifolia]

[Solanum tuberosum]

Seq. No. 234867
 Seq. ID LIB3272-044-P1-K1-C2
 Method BLASTX
 NCBI GI g2982268
 BLAST score 348
 E value 6.0e-33
 Match length 75
 % identity 91
 NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No. 234868
 Seq. ID LIB3272-044-P1-K1-C4
 Method BLASTX
 NCBI GI g3212869
 BLAST score 449
 E value 9.0e-45
 Match length 118
 % identity 69
 NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 234869
 Seq. ID LIB3272-044-P1-K1-C7
 Method BLASTX
 NCBI GI g481236
 BLAST score 265
 E value 3.0e-23
 Match length 64
 % identity 81
 NCBI Description hypothetical protein - Madagascar periwinkle
 >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
 [Catharanthus roseus]

Seq. No. 234870
 Seq. ID LIB3272-044-P1-K1-C8
 Method BLASTX
 NCBI GI g2677830
 BLAST score 525
 E value 1.0e-53
 Match length 112
 % identity 93
 NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No. 234871
 Seq. ID LIB3272-044-P1-K1-D1
 Method BLASTX
 NCBI GI g4263712
 BLAST score 302
 E value 1.0e-27
 Match length 80
 % identity 70
 NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 234872

0964016-103000

```
Seq. No.      234878
Seq. ID      LIB3272-044-P1-K1-E11
Method       BLASTX
NCBI GI      g2760320
BLAST score   301
E value      1.0e-27
Match length  94
% identity    67
NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]
```

```
Seq. No.      234879
Seq. ID       LIB3272-044-P1-K1-E2
Method        BLASTX
NCBI GI       g167367
BLAST score   313
E value       4.0e-29
Match length  80
% identity    81
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
```

```
Seq. No.          234880
Seq. ID           LIB3272-044-P1-K1-E3
Method            BLASTX
NCBI GI           g3132675
BLAST score       585
E value           9.0e-61
Match length      117
% identity         93
NCBI Description   (AF061740) asparagine synthetase [Elaeagnus umbellata]
```

Seq. No.	234881
Seq. ID	LIB3272-044-P1-K1-E5
Method	BLASTX
NCBI GI	g2462761
BLAST score	184
E value	3.0e-16
Match length	70
% identity	60
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

```
Seq. No.      234882
Seq. ID      LIB3272-044-P1-K1-E7
Method       BLASTX
NCBI GI      q3122785
```


BLAST score 267
 E value 1.0e-23
 Match length 79
 % identity 73
 NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No. 234883
 Seq. ID LIB3272-044-P1-K1-E8
 Method BLASTX
 NCBI GI g549063
 BLAST score 163
 E value 5.0e-17
 Match length 70
 % identity 71
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No. 234884
 Seq. ID LIB3272-044-P1-K1-E9
 Method BLASTX
 NCBI GI g2462753
 BLAST score 150
 E value 8.0e-10
 Match length 34
 % identity 79
 NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 234885
 Seq. ID LIB3272-044-P1-K1-F1
 Method BLASTX
 NCBI GI g2995384
 BLAST score 233
 E value 1.0e-19
 Match length 87
 % identity 62
 NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No. 234886
 Seq. ID LIB3272-044-P1-K1-F11
 Method BLASTX
 NCBI GI g266567
 BLAST score 202
 E value 8.0e-16
 Match length 62
 % identity 58
 NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir_S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi_21493_emb_CAA46990 (X66284) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No. 234887

NCBI GI g549063
 BLAST score 512
 E value 4.0e-52
 Match length 117
 % identity 83..
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1072464_pir_A38958 IgE-dependent histamine-releasing
 factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
 21kd polypeptide [Oryza sativa]

Seq. No. 234893
 Seq. ID LIB3272-044-P1-K1-G5
 Method BLASTX
 NCBI GI g2811025
 BLAST score 277
 E value 1.0e-24
 Match length 94
 % identity 62
 NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
 (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 234894
 Seq. ID LIB3272-044-P1-K1-G8
 Method BLASTX
 NCBI GI g4432840
 BLAST score 192
 E value 1.0e-14
 Match length 82
 % identity 51
 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 234895
 Seq. ID LIB3272-044-P1-K1-G9
 Method BLASTX
 NCBI GI g1710585
 BLAST score 362
 E value 1.0e-34
 Match length 84
 % identity 85
 NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_1143507_emb_CAA63786_
 (X93587) P0 ribosomal protein [Lupinus luteus]

Seq. No. 234896
 Seq. ID LIB3272-044-P1-K1-H11
 Method BLASTX
 NCBI GI g1666228
 BLAST score 263
 E value 2.0e-34
 Match length 91
 % identity 77
 NCBI Description (U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin
 [Pisum sativum] >gi_1724137 (U81046) actin [Pisum sativum]
 >gi_1724139 (U81047) actin [Pisum sativum]

Seq. No. 234897
 Seq. ID LIB3272-044-P1-K1-H12
 Method BLASTX


```
Method BLASTX
NCBI GI g421923
BLAST score 414
E value 1.0e-40
Match length 101
% identity 70
NCBI Description pathogenesis-related protein P23 - tomato (fragment)
>gi_542031_pir_PQ0742 pathogenesis-related protein P23
precursor - tomato (fragment) >gi_19315_emb_CAA50059_
(X70787) pathogenesis-related protein PR P23 [Lycopersicon
esculentum]
```

```
Seq. No.      234923
Seq. ID       LIB3272-045-P1-K1-D9
Method        BLASTX
NCBI GI       g3860323
BLAST score    374
E value        6.0e-36
Match length   78
% identity     87
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
```

```
Seq. No.      234924
Seq. ID      LIB3272-045-P1-K1-E1
Method       BLASTX
NCBI GI      g3319882
BLAST score   367
E value      2.0e-35
Match length  99
% identity    71
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
arietinum]
```

```
Seq. No.          234925
Seq. ID           LIB3272-045-P1-K1-E11
Method            BLASTX
NCBI GI           g629597
BLAST score       349
E value           5.0e-33
Match length      83
% identity        77
NCBI Description   proline-rich protein - rape >gi_545029_bbs_142669 (S68113)
                  proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                  Peptide, 147 aa] [Brassica napus]
```

```
Seq. No.      234926
Seq. ID       LIB3272-045-P1-K1-E2
Method        BLASTX
NCBI GI       g3402279
BLAST score    600
E value       2.0e-62
Match length   127
% identity     87
NCBI Description (AJ000999) putative beta-subunit of K+ channels [Solanum
tuberosum]
```

Seq. No. 234927


```

E value          3.0e-68
Match length     126
% identity       98
NCBI Description (U68461) actin [Striga asiatica]

```

```
Seq. No.      234933
Seq. ID      LIB3272-045-P1-K1-F2
Method       BLASTX
NCBI GI      g729470
BLAST score   400
E value      4.0e-39
Match length  102
% identity    75
NCBI Description  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                  (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                  (Z21493) mitochondrial formate dehydrogenase precursor
                  [Solanum tuberosum]
```

```

Seq. No.      234935
Seq. ID       LIB3272-045-P1-K1-F5
Method        BLASTX
NCBI GI       g113116
BLAST score   443
E value       5.0e-44
Match length  143
% identity    59
NCBI Description  ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
>gi_111396_pir_A35007 ATP citrate (pro-S)-lyase (EC
4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
[Rattus norvegicus]

```

```
Seq. No.      234937
Seq. ID      LIB3272-045-P1-K1-G1
Method      BLASTX
NCBI GI      q136251
```


% identity 92
NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal protein S14 [Lupinus luteus]

Seq. No. 234948
Seq. ID LIB3272-045-P1-K1-H9
Method BLASTX
NCBI GI g3320120
BLAST score 158
E value 9.0e-11
Match length 98
% identity 34
NCBI Description (U66669) 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo sapiens]

Seq. No. 234949
Seq. ID LIB3272-046-P1-K1-A11
Method BLASTX
NCBI GI g3721540
BLAST score 295
E value 1.0e-26
Match length 104
% identity 63
NCBI Description (D83583) Sulfite Reductase [Nicotiana tabacum]
>gi_3738234_dbj_BAA33796_ (AB010717) sulfite reductase [Nicotiana tabacum]

Seq. No. 234950
Seq. ID LIB3272-046-P1-K1-A12
Method BLASTX
NCBI GI g2388570
BLAST score 149
E value 2.0e-09
Match length 110
% identity 36
NCBI Description (AC000098) YUP8H12.12 [Arabidopsis thaliana]

Seq. No. 234951
Seq. ID LIB3272-046-P1-K1-A2
Method BLASTX
NCBI GI g2191131
BLAST score 188
E value 2.0e-14
Match length 55
% identity 67
NCBI Description (AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]

Seq. No. 234952
Seq. ID LIB3272-046-P1-K1-A4
Method BLASTX
NCBI GI g2924520
BLAST score 500
E value 1.0e-50
Match length 124
% identity 79
NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]


```
Seq. No.          234953
Seq. ID           LIB3272-046-P1-K1-A5
Method            BLASTX
NCBI GI           g1838976
BLAST score       279
E value           9.0e-25
Match length      147
% identity        43
NCBI Description   (X73635) vsf-1 [Lycopersicon esculentum]
```

```
Seq. No.      234954
Seq. ID      LIB3272-046-P1-K1-A6
Method       BLASTX
NCBI GI      g3236253
BLAST score   658
E value      3.0e-69
Match length  143
% identity    85
NCBI Description (AC004684) receptor-like protein kinase [Arabidopsis
thaliana]
```

```
Seq. No.      234955
Seq. ID      LIB3272-046-P1-K1-B1
Method       BLASTX
NCBI GI      g433970
BLAST score   128
E value      9.0e-16
Match length  116
% identity    8
NCBI Description (Z28649) polyubiquitin [Acetabularia cliftonii]
```

Seq. No.	234956
Seq. ID	LIB3272-046-P1-K1-B10
Method	BLASTX
NCBI GI	g1545805
BLAST score	157
E value	4.0e-11
Match length	51
% identity	65
NCBI Description	(D64052) cytochrome P450 like TBP [Nicotiana tabacum]

```

Seq. No.      234957
Seq. ID       LIB3272-046-P1-K1-B11
Method        BLASTX
NCBI GI       g303730
BLAST score    533
E value       2.0e-54
Match length   121
% identity     86
NCBI Description (D12540) GTP-binding protein [Pisum sativum]
                >gi_738933_prf__2001457A GTP-binding protein [Pisum
                sativum]

```

Seq. No.	234958
Seq. ID	LIB3272-046-P1-K1-B12
Method	BLASTX

Method	BLASTX
NCBI GI	g2088651
BLAST score	276
E value	2.0e-24
Match length	125
% identity	41
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]
Seq. No.	234974
Seq. ID	LIB3272-046-P1-K1-D7
Method	BLASTX
NCBI GI	g3901014
BLAST score	234
E value	1.0e-19
Match length	55
% identity	76
NCBI Description	(AJ130886) metallothionein-like protein class II [Fagus sylvatica]
Seq. No.	234975
Seq. ID	LIB3272-046-P1-K1-D8
Method	BLASTX
NCBI GI	g3915031
BLAST score	453
E value	3.0e-45
Match length	128
% identity	70
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232_ (X95988) delta 9 stearyl-[acyl-carrier protein] desaturase [Gossypium hirsutum]
Seq. No.	234976
Seq. ID	LIB3272-046-P1-K1-E1
Method	BLASTX
NCBI GI	g1065515
BLAST score	188
E value	4.0e-14
Match length	79
% identity	44
NCBI Description	(U40420) weak similarity to procollagen alpha chain 1(V) chain [Caenorhabditis elegans]
Seq. No.	234977
Seq. ID	LIB3272-046-P1-K1-E10
Method	BLASTX
NCBI GI	g131754
BLAST score	308
E value	4.0e-28
Match length	126
% identity	46
NCBI Description	PPLZ02 PROTEIN >gi_99973_pir_S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_ (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]

BLAST score 582
 E value 3.0e-60
 Match length 137
 % identity 83
 NCBI Description HEMOGLOBIN II >gi_99509_pir_S13378 hemoglobin II - swamp oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina glauca]

Seq. No. 234984
 Seq. ID LIB3272-046-P1-K1-F10
 Method BLASTX
 NCBI GI g3668082
 BLAST score 292
 E value 3.0e-26
 Match length 115
 % identity 55
 NCBI Description (AC004667) putative DAL1 protein [Arabidopsis thaliana]

Seq. No. 234985
 Seq. ID LIB3272-046-P1-K1-F2
 Method BLASTX
 NCBI GI g3341695
 BLAST score 537
 E value 5.0e-55
 Match length 147
 % identity 67
 NCBI Description (AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]

Seq. No. 234986
 Seq. ID LIB3272-046-P1-K1-F4
 Method BLASTX
 NCBI GI g3660467
 BLAST score 398
 E value 9.0e-39
 Match length 103
 % identity 78
 NCBI Description (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]

Seq. No. 234987
 Seq. ID LIB3272-046-P1-K1-F6
 Method BLASTX
 NCBI GI g1709498
 BLAST score 528
 E value 5.0e-54
 Match length 120
 % identity 79
 NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No. 234988
 Seq. ID LIB3272-046-P1-K1-F9
 Method BLASTX
 NCBI GI g3550985

Method BLASTX
 NCBI GI g543905
 BLAST score 392
 E value 5.0e-38
 Match length 125
 % identity 63
 NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
 brassinosteroid-regulated protein [Glycine max]

Seq. No. 234994
 Seq. ID LIB3272-046-P1-K1-H1
 Method BLASTX
 NCBI GI g4539335
 BLAST score 312
 E value 1.0e-28
 Match length 144
 % identity 46
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 234995
 Seq. ID LIB3272-046-P1-K1-H11
 Method BLASTX
 NCBI GI g3935152
 BLAST score 471
 E value 3.0e-47
 Match length 124
 % identity 69
 NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No. 234996
 Seq. ID LIB3272-046-P1-K1-H12
 Method BLASTX
 NCBI GI g3551838
 BLAST score 521
 E value 3.0e-53
 Match length 120
 % identity 84
 NCBI Description (AF070967) SKP1-like protein [Nicotiana glauca]

Seq. No. 234997
 Seq. ID LIB3272-046-P1-K1-H4
 Method BLASTX
 NCBI GI g1155261
 BLAST score 367
 E value 2.0e-42
 Match length 113
 % identity 82
 NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No. 234998
 Seq. ID LIB3272-046-P1-K1-H5
 Method BLASTX
 NCBI GI g2529229
 BLAST score 441
 E value 9.0e-44
 Match length 106


```
Seq. No.      235004
Seq. ID       LIB3272-047-P1-K1-A7
Method        BLASTX
NCBI GI       g3395423
BLAST score    300
E value        3.0e-27
Match length   117
% identity     56
NCBI Description (AC004683) putative protein kinase [Arabidopsis thaliana]
               >gi_3786023 (AC005499) putative protein kinase [Arabidopsis
               thaliana]
```

```
Seq. No.      235005
Seq. ID       LIB3272-047-P1-K1-A8
Method        BLASTX
NCBI GI       g3319882
BLAST score    496
E value       3.0e-50
Match length   101
% identity     92
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
arietinum]
```

```
Seq. No.      235006
Seq. ID      LIB3272-047-P1-K1-A9
Method       BLASTX
NCBI GI      g1709498
BLAST score   506
E value      2.0e-51
Match length 109
% identity    83
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
                thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                [Arabidopsis thaliana]
```

Seq. No.	235007
Seq. ID	LIB3272-047-P1-K1-B1
Method	BLASTX
NCBI GI	g2982331
BLAST score	578
E value	6.0e-60
Match length	118
% identity	97
NCBI Description	(AF051251) TAT-binding protein homolog [Picea mariana]

```
Seq. No.      235008
Seq. ID       LIB3272-047-P1-K1-B10
Method        BLASTX
NCBI GI       g1737492
BLAST score    407
E value        6.0e-40
Match length   103
% identity     82
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
```

Seq. No. 235009

E value 9.0e-35
 Match length 100
 % identity 70
 NCBI Description (AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]

Seq. No. 235020
 Seq. ID LIB3272-047-P1-K1-C2
 Method BLASTX
 NCBI GI g4455169
 BLAST score 306
 E value 4.0e-28
 Match length 116
 % identity 53
 NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No. 235021
 Seq. ID LIB3272-047-P1-K1-C3
 Method BLASTX
 NCBI GI g1166450
 BLAST score 295
 E value 1.0e-26
 Match length 63
 % identity 84
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

Seq. No. 235022
 Seq. ID LIB3272-047-P1-K1-C7
 Method BLASTX
 NCBI GI g3183207
 BLAST score 371
 E value 1.0e-35
 Match length 119
 % identity 55
 NCBI Description HYPOTHETICAL PROTEIN KIAA0017 >gi_285999_dbj_BAA02805_ (D13642) KIAA0017 [Homo sapiens]

Seq. No. 235023
 Seq. ID LIB3272-047-P1-K1-C8
 Method BLASTX
 NCBI GI g2244979
 BLAST score 402
 E value 3.0e-39
 Match length 118
 % identity 68
 NCBI Description (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No. 235024
 Seq. ID LIB3272-047-P1-K1-D12
 Method BLASTX
 NCBI GI g1172995
 BLAST score 213
 E value 4.0e-17
 Match length 89
 % identity 51

Seq. No.	235029
Seq. ID	LIB3272-047-P1-K1-D6
Method	BLASTX
NCBI GI	g2286153
BLAST score	554
E value	4.0e-57
Match length	112
% identity	99
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.	235030
Seq. ID	LIB3272-047-P1-K1-D7
Method	BLASTX
NCBI GI	g1864017
BLAST score	313
E value	4.0e-55
Match length	123
% identity	89
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.	235031
Seq. ID	LIB3272-047-P1-K1-D8
Method	BLASTX
NCBI GI	g3024020
BLAST score	498
E value	1.0e-50
Match length	104
% identity	89
NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanium tuberosum]
Seq. No.	235032
Seq. ID	LIB3272-047-P1-K1-D9
Method	BLASTX
NCBI GI	g4128197
BLAST score	172
E value	3.0e-14
Match length	65
% identity	62
NCBI Description	(U75273) acyl-CoA binding protein [Arabidopsis thaliana]
Seq. No.	235033
Seq. ID	LIB3272-047-P1-K1-E10
Method	BLASTX
NCBI GI	g1313972
BLAST score	294
E value	1.0e-26
Match length	118
% identity	53
NCBI Description	(Z72428) major allergen Mal d1 [Malus domestica]
Seq. No.	235034
Seq. ID	LIB3272-047-P1-K1-E11
Method	BLASTX
NCBI GI	g2935298
BLAST score	622

NCBI GI g167367
 BLAST score 461
 E value 3.0e-46
 Match length 120
 % identity 75
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 235056
 Seq. ID LIB3272-047-P1-K1-H7
 Method BLASTX
 NCBI GI g1922938
 BLAST score 189
 E value 2.0e-14
 Match length 105
 % identity 39
 NCBI Description (AC000106) Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb_Z29094). [Arabidopsis thaliana]

Seq. No. 235057
 Seq. ID LIB3272-047-P1-K1-H9
 Method BLASTX
 NCBI GI g1332579
 BLAST score 420
 E value 4.0e-45
 Match length 107
 % identity 9
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 235058
 Seq. ID LIB3272-048-P1-K1-A1
 Method BLASTX
 NCBI GI g232031
 BLAST score 197
 E value 2.0e-15
 Match length 77
 % identity 52
 NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No. 235059
 Seq. ID LIB3272-048-P1-K1-A10
 Method BLASTX
 NCBI GI g1353193
 BLAST score 175
 E value 9.0e-13
 Match length 100
 % identity 45
 NCBI Description O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir_JQ2268 O-methyltransferase (EC 2.1.1.-) - maize >gi_404070 (L14063) O-methyltransferase [Zea mays]

Seq. No. 235060
 Seq. ID LIB3272-048-P1-K1-A12
 Method BLASTX
 NCBI GI g2499945

Seq. No.	235075
Seq. ID	LIB3272-048-P1-K1-D11
Method	BLASTX
NCBI GI	g4314370
BLAST score	599
E value	2.0e-62
Match length	132
% identity	85
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.	235076
Seq. ID	LIB3272-048-P1-K1-D12
Method	BLASTX
NCBI GI	g2369714
BLAST score	651
E value	2.0e-68
Match length	129
% identity	94
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.	235077
Seq. ID	LIB3272-048-P1-K1-D4
Method	BLASTX
NCBI GI	g629806
BLAST score	600
E value	2.0e-62
Match length	115
% identity	94
NCBI Description	tubulin beta chain - rice >gi_493725_emb_CAA55912_ (X79367) beta tubulin [Oryza sativa]
Seq. No.	235078
Seq. ID	LIB3272-048-P1-K1-D6
Method	BLASTX
NCBI GI	g2827559
BLAST score	160
E value	7.0e-11
Match length	42
% identity	71
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	235079
Seq. ID	LIB3272-048-P1-K1-D7
Method	BLASTX
NCBI GI	g3603456
BLAST score	511
E value	4.0e-52
Match length	105
% identity	30
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]
Seq. No.	235080
Seq. ID	LIB3272-048-P1-K1-D9
Method	BLASTX

% identity 59
NCBI Description (AC005395) putative Cys3His zinc finger protein
[Arabidopsis thaliana]

Seq. No. 235096
Seq. ID LIB3272-048-P1-K1-G3
Method BLASTX
NCBI GI g464986
BLAST score 405
E value 1.0e-39
Match length 78
% identity 95
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
>gi_421857_pir_S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
>gi_297884_emb_CAA78714_(Z14990) ubiquitin conjugating
enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
ubiquitin conjugating enzyme [Arabidopsis thaliana]
>gi_600391_emb_CAA51201_(X72626) ubiquitin conjugating
enzyme E2 [Arabidopsis thaliana]
>gi_4455355_emb_CAB36765.1_(AL035524) ubiquitin-protein
ligase UBC9 [Arabidopsis thaliana]

Seq. No. 235097
Seq. ID LIB3272-048-P1-K1-G4
Method BLASTX
NCBI GI g3024020
BLAST score 627
E value 1.0e-65
Match length 125
% identity 94
NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
>gi_2225881_dbj_BAA20877_(AB004824) eukaryotic initiation
factor 5A3 [Solanum tuberosum]

Seq. No. 235098
Seq. ID LIB3272-048-P1-K1-G7
Method BLASTX
NCBI GI g3786016
BLAST score 326
E value 2.0e-30
Match length 131
% identity 55
NCBI Description (AC005499) putative elongation factor [Arabidopsis
thaliana]

Seq. No. 235099
Seq. ID LIB3272-048-P1-K1-G9
Method BLASTX
NCBI GI g3901014
BLAST score 235
E value 1.0e-19
Match length 55
% identity 76
NCBI Description (AJ130886) metallothionein-like protein class II [Fagus
sylvatica]


```
BLAST score      658
E value         3.0e-69
Match length    127
% identity      99
NCBI Description translation elongation factor eEF-1 alpha chain - maize
(fragment)
```

Seq. No.	235111
Seq. ID	LIB3272-049-P1-K1-A7
Method	BLASTX
NCBI GI	g1519680
BLAST score	167
E value	1.0e-11
Match length	127
% identity	31
NCBI Description	(U67953) contains similarity to C3HC4-class zinc finger (PS:PS00518) [Caenorhabditis elegans]

```
Seq. No.      235112
Seq. ID       LIB3272-049-P1-K1-A8
Method        BLASTX
NCBI GI       g169913
BLAST score    403
E value       2.0e-39
Match length   128
% identity     59
NCBI Description (M92090) beta-amylase [Glycine max]
```

```
Seq. No.      235113
Seq. ID      LIB3272-049-P1-K1-B11
Method       BLASTX
NCBI GI      g1888485
BLAST score   435
E value      4.0e-43
Match length  98
% identity    83
NCBI Description (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
```

Seq. No.	235114
Seq. ID	LIB3272-049-P1-K1-B12
Method	BLASTX
NCBI GI	g3643609
BLAST score	414
E value	1.0e-40
Match length	126
% identity	67
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

```
Seq. No.          235115
Seq. ID           LIB3272-049-P1-K1-B2
Method            BLASTX
NCBI GI           g2829133
BLAST score       148
E value           2.0e-09
Match length      102
% identity        35
```


>gi_282883_pir_S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana]
>gi_2842492_emb_CAA16889 (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 235136
Seq. ID LIB3272-049-P1-K1-E11
Method BLASTX
NCBI GI g3169182
BLAST score 313
E value 7.0e-29
Match length 78
% identity 76
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 235137
Seq. ID LIB3272-049-P1-K1-E12
Method BLASTX
NCBI GI g1173256
BLAST score 535
E value 7.0e-55
Match length 108
% identity 94
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No. 235138
Seq. ID LIB3272-049-P1-K1-E2
Method BLASTX
NCBI GI g3281861
BLAST score 216
E value 2.0e-17
Match length 107
% identity 44
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 235139
Seq. ID LIB3272-049-P1-K1-E4
Method BLASTX
NCBI GI g543905
BLAST score 427
E value 3.0e-42
Match length 103
% identity 82
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No. 235140
Seq. ID LIB3272-049-P1-K1-E5
Method BLASTX
NCBI GI g100525
BLAST score 573
E value 2.0e-59
Match length 115

E value 2.0e-45
 Match length 118
 % identity 80
 NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No. 235146
 Seq. ID LIB3272-049-P1-K1-F9
 Method BLASTX
 NCBI GI g1173256
 BLAST score 567
 E value 1.0e-58
 Match length 108
 % identity 100
 NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir_S45026 ribosomal protein S4 - upland cotton >gi_488739_emb_CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]

Seq. No. 235147
 Seq. ID LIB3272-049-P1-K1-G1
 Method BLASTX
 NCBI GI g1657948
 BLAST score 538
 E value 3.0e-55
 Match length 117
 % identity 89
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 235148
 Seq. ID LIB3272-049-P1-K1-G7
 Method BLASTX
 NCBI GI g1495366
 BLAST score 424
 E value 7.0e-42
 Match length 89
 % identity 83
 NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 235149
 Seq. ID LIB3272-049-P1-K1-G8
 Method BLASTX
 NCBI GI g3549691
 BLAST score 431
 E value 1.0e-42
 Match length 98
 % identity 73
 NCBI Description (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]

Seq. No. 235150
 Seq. ID LIB3272-049-P1-K1-H10
 Method BLASTX
 NCBI GI g4210948
 BLAST score 481
 E value 2.0e-48
 Match length 100
 % identity 92

E value	1.0e-18
Match length	47
% identity	91
NCBI Description	WOUND-INDUCED BASIC PROTEIN >gi_81888_pir_JS0731 wound-inducible basic protein - kidney bean >gi_169365 (L00625) basic protein [Phaseolus vulgaris] >gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein [Phaseolus vulgaris]
Seq. No.	235157
Seq. ID	LIB3272-050-P1-K1-A12
Method	BLASTX
NCBI GI	g3123271
BLAST score	453
E value	3.0e-45
Match length	105
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.	235158
Seq. ID	LIB3272-050-P1-K1-A3
Method	BLASTX
NCBI GI	g1155261
BLAST score	523
E value	2.0e-53
Match length	118
% identity	86
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]
Seq. No.	235159
Seq. ID	LIB3272-050-P1-K1-A5
Method	BLASTX
NCBI GI	g3687237
BLAST score	349
E value	4.0e-33
Match length	117
% identity	62
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]
Seq. No.	235160
Seq. ID	LIB3272-050-P1-K1-A9
Method	BLASTX
NCBI GI	g1928981
BLAST score	527
E value	6.0e-54
Match length	114
% identity	92
NCBI Description	(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]
Seq. No.	235161
Seq. ID	LIB3272-050-P1-K1-B10
Method	BLASTX
NCBI GI	g2501578


```
E value      1.0e-22
Match length 103
% identity   56
NCBI Description MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR
>gi_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana]
>gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis
mitochondrion-localized small heat shock protein
(AtHSP23.6-mito) [Arabidopsis thaliana]
```

```
Seq. No.      235167
Seq. ID      LIB3272-050-P1-K1-B6
Method       BLASTX
NCBI GI      g1172995
BLAST score   235
E value      1.0e-19
Match length  94
% identity    54
NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
ribosomal protein L22 [Rattus norvegicus]
>gi_1093952_prf__2105193A ribosomal protein L22 [Rattus
norvegicus]
```

```
Seq. No.      235168
Seq. ID      LIB3272-050-P1-K1-B7
Method       BLASTX
NCBI GI      g125606
BLAST score   431
E value      1.0e-42
Match length  95
% identity    85
NCBI Description  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
pyruvate kinase (EC 2.7.1.40) - potato
>gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
tuberosum]
```

```
Seq. No.      235169
Seq. ID       LIB3272-050-P1-K1-C1
Method        BLASTX
NCBI†GI       g4530585
BLAST score    357
E value        4.0e-34
Match length   85
% identity     74
NCBI Description (AF130978) B12D protein [Ipomoea batatas]
```

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Seq. No.      235170
Seq: ID       LIB3272-050-P1-K1-C10
Method        BLASTX
NCBI GI       g1709498
BLAST score    506
E value       2.0e-51
Match length  109
% identity    83
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                >gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
                thaliana >gi_887390_emb_CAA61411 (X89008) osmotin
```


[*Arabidopsis thaliana*]

Seq. No. 235171
 Seq. ID LIB3272-050-P1-K1-C11
 Method BLASTX
 NCBI GI g3377797
 BLAST score 458
 E value 7.0e-46
 Match length 118
 % identity 76
 NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara]

Seq. No. 235172
 Seq. ID LIB3272-050-P1-K1-C2
 Method BLASTX
 NCBI GI g1172977
 BLAST score 540
 E value 2.0e-55
 Match length 127
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [*Arabidopsis thaliana*]

Seq. No. 235173
 Seq. ID LIB3272-050-P1-K1-C3
 Method BLASTX
 NCBI GI g1666234
 BLAST score 472
 E value 2.0e-47
 Match length 88
 % identity 100
 NCBI Description (U76193) actin [*Pisum sativum*] >gi_1724143 (U81049) actin [*Pisum sativum*]

Seq. No. 235174
 Seq. ID LIB3272-050-P1-K1-C7
 Method BLASTX
 NCBI GI g3024017
 BLAST score 465
 E value 1.0e-46
 Match length 101
 % identity 92
 NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation initiation factor eIF-1A [*Onobrychis viciifolia*]

Seq. No. 235175
 Seq. ID LIB3272-050-P1-K1-C9
 Method BLASTX
 NCBI GI g2677828
 BLAST score 399
 E value 6.0e-39
 Match length 122


```
% identity      66
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
```

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Seq. No.      235176
Seq. ID      LIB3272-050-P1-K1-D10
Method       BLASTX
NCBI GI      g125606
BLAST score   443
E value      4.0e-44
Match length  94
% identity    88
NCBI Description  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248
pyruvate kinase (EC 2.7.1.40) - potato
>gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
tuberosum]
```

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Seq. No.          235178
Seq. ID           LIB3272-050-P1-K1-D4
Method            BLASTX
NCBI GI           g3694872
BLAST score       429
E value           2.0e-42
Match length      105
% identity        78
NCBI Description   (AF092547) profilin [Ricinus communis]
```

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Seq. No.          235180
Seq. ID           LIB3272-050-P1-K1-D7
Method            BLASTX
NCBI GI           g3851636
BLAST score       515
E value           2.0e-52
Match length      115
% identity        84
```


NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224
translation elongation factor eEF-1 beta' chain - rice
>gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
[Oryza sativa]

Seq. No. 235186
Seq. ID LIB3272-050-P1-K1-E5
Method BLASTX
NCBI GI g3687237
BLAST score 319
E value 1.0e-29
Match length 123
% identity 58
NCBI Description (AC005169) putative Cys3His zinc-finger protein
[Arabidopsis thaliana]

Seq. No. 235187
Seq. ID LIB3272-050-P1-K1-E6
Method BLASTX
NCBI GI g1173187
BLAST score 471
E value 2.0e-47
Match length 109
% identity 83
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir_S56673
ribosomal protein S23.e, cytosolic (clone RJ3) - garden
strawberry >gi_643074 (U19940) putative 40S ribosomal
protein s12 [Fragaria x ananassa]

Seq. No. 235188
Seq. ID LIB3272-050-P1-K1-E7
Method BLASTX
NCBI GI g1928981
BLAST score 549
E value 2.0e-56
Match length 114
% identity 95
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
oleracea var. botrytis]

Seq. No. 235189
Seq. ID LIB3272-050-P1-K1-E9
Method BLASTX
NCBI GI g508304
BLAST score 277
E value 1.0e-24
Match length 66
% identity 79
NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 235190
Seq. ID LIB3272-050-P1-K1-F1
Method BLASTX
NCBI GI g2130073
BLAST score 186
E value 5.0e-14
Match length 78

% identity 99
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
 (M88324) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167347 (M37697) Lea5-A late
 embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235252
 Seq. ID LIB3272-051-P1-K1-G3
 Method BLASTX
 NCBI GI g832876
 BLAST score 580
 E value 4.0e-60
 Match length 126
 % identity 90
 NCBI Description (L41345) ascorbate free radical reductase [Solanum
 lycopersicum] >gi_1097368_prf_2113407A ascorbate free
 radical reductase [Lycopersicon esculentum]

Seq. No. 235253
 Seq. ID LIB3272-051-P1-K1-G6
 Method BLASTX
 NCBI GI g2160156
 BLAST score 399
 E value 6.0e-39
 Match length 96
 % identity 74
 NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA
 synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No. 235254
 Seq. ID LIB3272-051-P1-K1-G8
 Method BLASTX
 NCBI GI g1166450
 BLAST score 321
 E value 1.0e-29
 Match length 71
 % identity 82
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]

Seq. No. 235255
 Seq. ID LIB3272-051-P1-K1-G9
 Method BLASTX
 NCBI GI g1332579
 BLAST score 430
 E value 4.0e-63
 Match length 137
 % identity 9
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 235256
 Seq. ID LIB3272-051-P1-K1-H1
 Method BLASTX
 NCBI GI g4262174
 BLAST score 305
 E value 7.0e-28
 Match length 132
 % identity 45

NCBI GI g2493144
 BLAST score 412
 E value 2.0e-40
 Match length 97
 % identity 57
 NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir_S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No. 235273
 Seq. ID LIB3272-052-P1-K1-A8
 Method BLASTX
 NCBI GI g4455364
 BLAST score 336
 E value 2.0e-31
 Match length 107
 % identity 59
 NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No. 235274
 Seq. ID LIB3272-052-P1-K1-A9
 Method BLASTX
 NCBI GI g4056469
 BLAST score 576
 E value 1.0e-59
 Match length 112
 % identity 100
 NCBI Description (AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No. 235275
 Seq. ID LIB3272-052-P1-K1-B11
 Method BLASTX
 NCBI GI g464981
 BLAST score 438
 E value 2.0e-43
 Match length 84
 % identity 95
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 235276
 Seq. ID LIB3272-052-P1-K1-B12
 Method BLASTX
 NCBI GI g1709498
 BLAST score 515
 E value 2.0e-52
 Match length 112
 % identity 83

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
>gi_1362001_pir_S57524 osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
[Arabidopsis thaliana]

Seq. No. 235277
Seq. ID LIB3272-052-P1-K1-B2
Method BLASTX
NCBI GI g3319921
BLAST score 267
E value 2.0e-23
Match length 95
% identity 60
NCBI Description (AJ223388) Hev b 3 [Hevea brasiliensis]
>gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3
[Hevea brasiliensis] >gi_3818475 (AF051317) small rubber
particle protein [Hevea brasiliensis]

Seq. No. 235278
Seq. ID LIB3272-052-P1-K1-B3
Method BLASTX
NCBI GI g1076274
BLAST score 295
E value 1.0e-26
Match length 102
% identity 59
NCBI Description cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No. 235279
Seq. ID LIB3272-052-P1-K1-B4
Method BLASTX
NCBI GI g2495155
BLAST score 152
E value 6.0e-10
Match length 112
% identity 39
NCBI Description GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR).
>gi_1694926_dbj_BAA08910_ (D50407) glutamyl-tRNA reductase
[Cucumis sativus]

Seq. No. 235280
Seq. ID LIB3272-052-P1-K1-C10
Method BLASTX
NCBI GI g3377797
BLAST score 282
E value 3.0e-25
Match length 125
% identity 50
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for
by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
H36046; coded for by A. thaliana cDNA T44067; coded for by
A. thaliana cDNA T14056; coded for by A. thaliana cDNA
R90691 [Ara

Seq. No. 235281
Seq. ID LIB3272-052-P1-K1-C12

BLAST score 616
 E value 2.0e-64
 Match length 122
 % identity 94
 NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
 >gi_100345_pir_S21060 translation initiation factor eIF-5A
 - common tobacco >gi_19887_emb_CAA45105_ (X63543)
 eukaryotic initiation factor 5A (3) [Nicotiana tabacum]

Seq. No. 235302
 Seq. ID LIB3272-052-P1-K1-F10
 Method BLASTX
 NCBI GI g3168840
 BLAST score 298
 E value 4.0e-27
 Match length 74
 % identity 74
 NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 235303
 Seq. ID LIB3272-052-P1-K1-F12
 Method BLASTX
 NCBI GI g1657948
 BLAST score 574
 E value 2.0e-59
 Match length 127
 % identity 87
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 235304
 Seq. ID LIB3272-052-P1-K1-F2
 Method BLASTX
 NCBI GI g3786017
 BLAST score 264
 E value 4.0e-23
 Match length 112
 % identity 49
 NCBI Description (AC005499) putative non-green plastid inner envelope
 membrane protein [Arabidopsis thaliana]

Seq. No. 235305
 Seq. ID LIB3272-052-P1-K1-F3
 Method BLASTX
 NCBI GI g3269293
 BLAST score 281
 E value 4.0e-25
 Match length 90
 % identity 64
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 235306
 Seq. ID LIB3272-052-P1-K1-F4
 Method BLASTX
 NCBI GI g1657948
 BLAST score 457
 E value 1.0e-45
 Match length 116

% identity 78
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
 Seq. No. 235307
 Seq. ID LIB3272-052-P1-K1-F5
 Method BLASTX
 NCBI GI g1168196
 BLAST score 314
 E value 6.0e-29
 Match length 69
 % identity 88
 NCBI Description 14-3-3-LIKE PROTEIN >gi_555974 (U15036) 14-3-3-like protein [Pisum sativum]

Seq. No. 235308
 Seq. ID LIB3272-052-P1-K1-F8
 Method BLASTX
 NCBI GI g2811026
 BLAST score 372
 E value 1.0e-35
 Match length 80
 % identity 89
 NCBI Description TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi_1946375 (U93215) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >gi_2347204 (AC002338) TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]

Seq. No. 235309
 Seq. ID LIB3272-052-P1-K1-G1
 Method BLASTX
 NCBI GI g3894186
 BLAST score 294
 E value 1.0e-26
 Match length 116
 % identity 53
 NCBI Description (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]

Seq. No. 235310
 Seq. ID LIB3272-052-P1-K1-G10
 Method BLASTX
 NCBI GI g4210948
 BLAST score 571
 E value 5.0e-59
 Match length 109
 % identity 97
 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 235311
 Seq. ID LIB3272-052-P1-K1-G11
 Method BLASTX
 NCBI GI g4263712
 BLAST score 388
 E value 1.0e-37
 Match length 93
 % identity 77
 NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis

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NCBI GI	2661840
BLAST score	371
E value	1.0e-35
Match length	96
% identity	70
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.	235318
Seq. ID	LIB3272-052-P1-K1-H10
Method	BLASTX
NCBI GI	g4417280
BLAST score	265
E value	3.0e-23
Match length	70
% identity	77
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]
Seq. No.	235319
Seq. ID	LIB3272-052-P1-K1-H11
Method	BLASTX
NCBI GI	g417148
BLAST score	403
E value	2.0e-39
Match length	130
% identity	61
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir_A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]
Seq. No.	235320
Seq. ID	LIB3272-052-P1-K1-H3
Method	BLASTX
NCBI GI	g113621
BLAST score	439
E value	1.0e-43
Match length	102
% identity	86
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366 (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A cytoplasmic aldolase [Zea mays]
Seq. No.	235321
Seq. ID	LIB3272-052-P1-K1-H4
Method	BLASTX
NCBI GI	g266936
BLAST score	397
E value	1.0e-38
Match length	113
% identity	74
NCBI Description	50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27) >gi_282960_pir_A42840 ribosomal protein L27 - common tobacco >gi_170306 (M98473) ribosomal protein L27 [Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein L27 [Nicotiana tabacum]

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Seq. No.	235328
Seq. ID	LIB3272-053-P1-K1-A4
Method	BLASTX
NCBI GI	g2500354
BLAST score	683
E value	4.0e-72
Match length	132
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

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Seq. No.      235330
Seq. ID      LIB3272-053-P1-K1-A7
Method       BLASTX
NCBI GI      g4217999
BLAST score   475
E value      9.0e-48
Match length  116
% identity    81
NCBI Description (AC006135) putative ubiquitin--protein ligase
               (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
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Seq. No.      235331
Seq. ID       LIB3272-053-P1-K1-A8
Method        BLASTX
NCBI GI       g3885515
BLAST score    388
E value       9.0e-38
Match length   77
% identity     95
NCBI Description: (AF084202) similar to ribosomal protein S26 [Medicago
                  sativa]
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% identity      54
NCBI Description (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family). [Arabidopsis thaliana]

Seq. No.        235337
Seq. ID         LIB3272-053-P1-K1-B7
Method          BLASTX
NCBI GI         g2780225
BLAST score     223
E value         2.0e-18
Match length    74
% identity      53
NCBI Description (AJ223281) alpha-hydroxynitrile lyase [Manihot esculenta]

Seq. No.        235338
Seq. ID         LIB3272-053-P1-K1-B8
Method          BLASTX
NCBI GI         g114420
BLAST score     181
E value         2.0e-13
Match length    70
% identity      54
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_100882_pir_S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >gi_22173_emb_CAA38140 (X54233) ATPase F1 subunit protein
                  [Zea mays] >gi_897618 (M36087) F-1-ATPase subunit 2 [Zea
                  mays]

Seq. No.        235339
Seq. ID         LIB3272-053-P1-K1-C11
Method          BLASTX
NCBI GI         g4098647
BLAST score     745
E value         2.0e-79
Match length    142
% identity      92
NCBI Description (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
                  thaliana]

Seq. No.        235340
Seq. ID         LIB3272-053-P1-K1-C3
Method          BLASTX
NCBI GI         g464986
BLAST score     541
E value         2.0e-55
Match length    104
% identity      96
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir_S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714 (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi_600391_emb_CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]

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Seq. No. 235371
 Seq. ID LIB3272-054-P1-K1-A1
 Method BLASTX
 NCBI GI g126770
 BLAST score 141
 E value 3.0e-09
 Match length 59
 % identity 49
 NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate synthase (EC 4.1.3.2) - upland cotton
 >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
 [Gossypium hirsutum]

Seq. No. 235372
 Seq. ID LIB3272-054-P1-K1-A10
 Method BLASTX
 NCBI GI g508304
 BLAST score 215
 E value 3.0e-17
 Match length 73
 % identity 60
 NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 235373
 Seq. ID LIB3272-054-P1-K1-A11
 Method BLASTX
 NCBI GI g2792297
 BLAST score 197
 E value 2.0e-15
 Match length 55
 % identity 60
 NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 235374
 Seq. ID LIB3272-054-P1-K1-A2
 Method BLASTX
 NCBI GI g167367
 BLAST score 436
 E value 3.0e-43
 Match length 123
 % identity 68
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 235375
 Seq. ID LIB3272-054-P1-K1-A5
 Method BLASTX
 NCBI GI g3759184
 BLAST score 331
 E value 6.0e-31
 Match length 135
 % identity 52
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 235376
 Seq. ID LIB3272-054-P1-K1-B10
 Method BLASTX

Match length	61
% identity	56
NCBI Description	(297336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	235381
Seq. ID	LIB3272-054-P1-K1-B9
Method	BLASTX
NCBI GI	g4090257
BLAST score	286
E value	8.0e-40
Match length	91
% identity	95
NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
Seq. No.	235382
Seq. ID	LIB3272-054-P1-K1-C1
Method	BLASTX
NCBI GI	g1545805
BLAST score	207
E value	2.0e-16
Match length	71
% identity	63
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]
Seq. No.	235383
Seq. ID	LIB3272-054-P1-K1-C11
Method	BLASTX
NCBI GI	g1419090
BLAST score	389
E value	1.0e-37
Match length	121
% identity	64
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]
Seq. No.	235384
Seq. ID	LIB3272-054-P1-K1-C2
Method	BLASTX
NCBI GI	g3337356
BLAST score	228
E value	7.0e-19
Match length	90
% identity	64
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]
Seq. No.	235385
Seq. ID	LIB3272-054-P1-K1-C3
Method	BLASTX
NCBI GI	g1724100
BLAST score	255
E value	2.0e-22
Match length	70
% identity	70
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]
Seq. No.	235386

Seq. ID LIB3272-054-P1-K1-C7
 Method BLASTX
 NCBI GI g3421102
 BLAST score 493
 E value 6.0e-50
 Match length 109
 % identity 83
 NCBI Description (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No. 235387
 Seq. ID LIB3272-054-P1-K1-C8
 Method BLASTX
 NCBI GI g4510363
 BLAST score 569
 E value 8.0e-59
 Match length 117
 % identity 87
 NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No. 235388
 Seq. ID LIB3272-054-P1-K1-D1
 Method BLASTX
 NCBI GI g1172555
 BLAST score 414
 E value 8.0e-41
 Match length 96
 % identity 83
 NCBI Description 34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) >gi_629720_pir_S46936 34K porin - potato >gi_1076682_pir_A55364 porin (clone pPOM-34) - potato mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDA porin [Solanum tuberosum]

Seq. No. 235389
 Seq. ID LIB3272-054-P1-K1-D12
 Method BLASTX
 NCBI GI g1351014
 BLAST score 232
 E value 1.0e-19
 Match length 76
 % identity 64
 NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No. 235390
 Seq. ID LIB3272-054-P1-K1-D2
 Method BLASTX
 NCBI GI g464981
 BLAST score 737
 E value 2.0e-78
 Match length 137
 % identity 98
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)

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Seq. No.	235396
Seq. ID	LIB3272-054-P1-K1-E2

Method BLASTX
 NCBI GI g4539292
 BLAST score 452
 E value 4.0e-45
 Match length 96
 % identity 86
 NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 235397
 Seq. ID LIB3272-054-P1-K1-E3
 Method BLASTX
 NCBI GI g2815246
 BLAST score 225
 E value 2.0e-18
 Match length 55
 % identity 73
 NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]

Seq. No. 235398
 Seq. ID LIB3272-054-P1-K1-E7
 Method BLASTX
 NCBI GI g2129495
 BLAST score 274
 E value 3.0e-24
 Match length 54
 % identity 89
 NCBI Description fiber protein E6 (clone SIE6-2A) - sea-island cotton
 >gi_1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
 (U30508) E6 [Gossypium barbadense]

Seq. No. 235399
 Seq. ID LIB3272-054-P1-K1-E9
 Method BLASTX
 NCBI GI g549063
 BLAST score 367
 E value 4.0e-35
 Match length 112
 % identity 65
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1072464_pir_A38958 IgE-dependent histamine-releasing
 factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
 21kd polypeptide [Oryza sativa]

Seq. No. 235400
 Seq. ID LIB3272-054-P1-K1-F11
 Method BLASTX
 NCBI GI g3450889
 BLAST score 253
 E value 9.0e-22
 Match length 60
 % identity 80
 NCBI Description (AF083890) 19S proteasome subunit 9 [Arabidopsis thaliana]

Seq. No. 235401
 Seq. ID LIB3272-054-P1-K1-F4
 Method BLASTX

% identity 55
 NCBI Description (Y11987) FPF1 protein [Sinapis alba]

Seq. No. 235407
 Seq. ID LIB3272-054-P1-K1-G10
 Method BLASTX
 NCBI GI g3860277
 BLAST score 400
 E value 5.0e-39
 Match length 95
 % identity 82
 NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 235408
 Seq. ID LIB3272-054-P1-K1-G3
 Method BLASTX
 NCBI GI g4519673
 BLAST score 696
 E value 1.0e-73
 Match length 140
 % identity 83
 NCBI Description (AB017694) WREBP-2 [Nicotiana tabacum]

Seq. No. 235409
 Seq. ID LIB3272-054-P1-K1-G8
 Method BLASTX
 NCBI GI g4204793
 BLAST score 636
 E value 1.0e-66
 Match length 135
 % identity 47
 NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]

Seq. No. 235410
 Seq. ID LIB3272-054-P1-K1-G9
 Method BLASTX
 NCBI GI g3158372
 BLAST score 436
 E value 2.0e-43
 Match length 90
 % identity 53
 NCBI Description (AF035383) polyubiquitin [Arabidopsis thaliana]

Seq. No. 235411
 Seq. ID LIB3272-054-P1-K1-H1
 Method BLASTX
 NCBI GI g120669
 BLAST score 497
 E value 2.0e-50
 Match length 99
 % identity 93
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde

0963016

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Seq. No.      235413
Seq. ID       LIB3272-054-P1-K1-H12
Method        BLASTX
NCBI GI       : g3860247
BLAST score    396
E value       2.0e-39
Match length   100
% identity     84
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
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Seq. No.      235415
Seq. ID      LIB3272-054-P1-K1-H9
Method       BLASTX
NCBI GI      gl20777
BLAST score   159
E value      9.0e-11
Match length  75
% identity   44
NCBI Description  SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)
>gi_147901 (M88334) succinic semialdehyde dehydrogenase
[Escherichia coli] >gi_1789015 (AE000351)
succinate-semialdehyde dehydrogenase, NADP-dependent
activity [Escherichia coli]
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34078

Seq. No. 235417
 Seq. ID LIB3272-055-P1-K1-A12
 Method BLASTX
 NCBI GI g629483
 BLAST score 228
 E value 9.0e-19
 Match length 115
 % identity 44
 NCBI Description gene 1-Sc3 protein - European white birch
 >gi_534898_emb_CAA54696_(X77601) 1 Sc-3 [Betula pendula]
 >gi_1584322_prf_2122374C allergen Bet v 1-Sc3 [Betula
 pendula]

Seq. No. 235418
 Seq. ID LIB3272-055-P1-K1-A3
 Method BLASTX
 NCBI GI g2982452
 BLAST score 250
 E value 1.0e-21
 Match length 113
 % identity 7
 NCBI Description (AL022223) receptor protein kinase-like protein
 [Arabidopsis thaliana]

Seq. No. 235419
 Seq. ID LIB3272-055-P1-K1-A5
 Method BLASTX
 NCBI GI g862931
 BLAST score 341
 E value 3.0e-32
 Match length 103
 % identity 68
 NCBI Description (U27179) acidic glucanase [Medicago sativa subsp. sativa]

Seq. No. 235420
 Seq. ID LIB3272-055-P1-K1-A6
 Method BLASTX
 NCBI GI g2462762
 BLAST score 341
 E value 4.0e-32
 Match length 126
 % identity 57
 NCBI Description (AC002292) Highly similar to auxin-induced protein
 (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 235421
 Seq. ID LIB3272-055-P1-K1-A7
 Method BLASTX
 NCBI GI g3915826
 BLAST score 456
 E value 1.0e-45
 Match length 119
 % identity 74
 NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 235422

Match length 76
 % identity 91
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
 (M88324) late embryogenesis-abundant protein [Gossypium
 hirsutum] >gi_167347 (M37697) Lea5-A late
 embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235439
 Seq. ID LIB3272-055-P1-K1-D2
 Method BLASTX
 NCBI GI g3281853
 BLAST score 181
 E value 3.0e-13
 Match length 37
 % identity 95
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 235440
 Seq. ID LIB3272-055-P1-K1-D5
 Method BLASTX
 NCBI GI g3482980
 BLAST score 326
 E value 3.0e-30
 Match length 140
 % identity 51
 NCBI Description (AL031369) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235441
 Seq. ID LIB3272-055-P1-K1-D7
 Method BLASTX
 NCBI GI g3241945
 BLAST score 192
 E value 1.0e-14
 Match length 109
 % identity 39
 NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

Seq. No. 235442
 Seq. ID LIB3272-055-P1-K1-E1
 Method BLASTX
 NCBI GI g167367
 BLAST score 406
 E value 1.0e-39
 Match length 109
 % identity 72
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 235443
 Seq. ID LIB3272-055-P1-K1-E10
 Method BLASTX
 NCBI GI g1621268
 BLAST score 379
 E value 1.0e-36
 Match length 114
 % identity 69
 NCBI Description (Z81012) unknown [Ricinus communis]

Method BLASTX
 NCBI GI g549063
 BLAST score 493
 E value 7.0e-50
 Match length 113
 % identity 82
 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 >gi_1072464_pir_A38958 IgE-dependent histamine-releasing
 factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
 21kd polypeptide [Oryza sativa]

Seq. No. 235450
 Seq. ID LIB3272-055-P1-K1-F6
 Method BLASTX
 NCBI GI g3868758
 BLAST score 484
 E value 8.0e-49
 Match length 136
 % identity 65
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 235451
 Seq. ID LIB3272-055-P1-K1-F7
 Method BLASTX
 NCBI GI g4210948
 BLAST score 514
 E value 2.0e-52
 Match length 100
 % identity 96
 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 235452
 Seq. ID LIB3272-055-P1-K1-F8
 Method BLASTX
 NCBI GI g3142698
 BLAST score 362
 E value 1.0e-34
 Match length 88
 % identity 78
 NCBI Description (AF064542) protein farnesyltransferase subunit A
 [Arabidopsis thaliana]

Seq. No. 235453
 Seq. ID LIB3272-055-P1-K1-F9
 Method BLASTX
 NCBI GI g2088651
 BLAST score 313
 E value 6.0e-29
 Match length 101
 % identity 61
 NCBI Description (AF002109) hypersensitivity-related gene 201 isolog
 [Arabidopsis thaliana]

Seq. No. 235454
 Seq. ID LIB3272-055-P1-K1-G1
 Method BLASTX
 NCBI GI g4567267

BLAST score 313
 E value 5.0e-43
 Match length 95
 % identity 60
 NCBI Description (AC006841) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 235455
 Seq. ID LIB3272-055-P1-K1-G10
 Method BLASTX
 NCBI GI g417103
 BLAST score 645
 E value 1.0e-67
 Match length 129
 % identity 100
 NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone H3.3-like protein - Arabidopsis thaliana
 >gi_16324_emb_CAA42957_(X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_(X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_(X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_(X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1 (AL035708) Histone H3 [Arabidopsis thaliana]

Seq. No. 235456
 Seq. ID LIB3272-055-P1-K1-G12
 Method BLASTX
 NCBI GI g2995384
 BLAST score 167
 E value 9.0e-12
 Match length 59
 % identity 57
 NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No. 235457
 Seq. ID LIB3272-055-P1-K1-G3
 Method BLASTX
 NCBI GI g464444
 BLAST score 466
 E value 7.0e-47
 Match length 100
 % identity 89
 NCBI Description PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 30 KD SUBUNIT) >gi_541889_pir_S39900 proteasome - Arabidopsis thaliana >gi_166830 (M98495) proteasome [Arabidopsis thaliana]

Seq. No. 235458
 Seq. ID LIB3272-055-P1-K1-G9
 Method BLASTX
 NCBI GI g2739168
 BLAST score 311
 E value 2.0e-36
 Match length 115
 % identity 67
 NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No. 235459
 Seq. ID LIB3272-055-P1-K1-H1
 Method BLASTX
 NCBI GI g4455207
 BLAST score 440
 E value 1.0e-43
 Match length 95
 % identity 91
 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 235460
 Seq. ID LIB3272-055-P1-K1-H10
 Method BLASTX
 NCBI GI g1076737
 BLAST score 414
 E value 8.0e-41
 Match length 81
 % identity 98
 NCBI Description beta-tubulin R1623 - rice

Seq. No. 235461
 Seq. ID LIB3272-055-P1-K1-H7
 Method BLASTX
 NCBI GI g4455207
 BLAST score 339
 E value 8.0e-32
 Match length 96
 % identity 75
 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 235462
 Seq. ID LIB3272-055-P1-K1-H8
 Method BLASTX
 NCBI GI g544437
 BLAST score 374
 E value 6.0e-36
 Match length 85
 % identity 86
 NCBI Description GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
 >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]

Seq. No. 235463
 Seq. ID LIB3272-055-P1-K1-H9
 Method BLASTX
 NCBI GI g3851636

Seq. ID LIB3272-058-P1-K1-A2
 Method BLASTX
 NCBI GI g1705812
 BLAST score 475
 E value 9.0e-48
 Match length 141
 % identity 64
 NCBI Description ACIDIC CHITINASE PRECURSOR >gi_1150686_emb_CAA92207_ (Z68123) acidic chitinase [Vitis vinifera]

Seq. No. 235468
 Seq. ID LIB3272-058-P1-K1-A3
 Method BLASTX
 NCBI GI g1170747
 BLAST score 385
 E value 3.0e-37
 Match length 87
 % identity 85
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235469
 Seq. ID LIB3272-058-P1-K1-A4
 Method BLASTX
 NCBI GI g2500347
 BLAST score 254
 E value 2.0e-26
 Match length 117
 % identity 60
 NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG >gi_3878691_emb_CAA90127 (Z49911) similar to ribosomal protein (L7AE family); cDNA EST EMBL:D73957 comes from this gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393 comes from this gene; cD

Seq. No. 235470
 Seq. ID LIB3272-058-P1-K1-A5
 Method BLASTX
 NCBI GI g136636
 BLAST score 543
 E value 9.0e-56
 Match length 105
 % identity 95
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir_S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No. 235471


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Seq. ID          LIB3272-058-P1-K1-D12
Method          BLASTX
NCBI GI         g1130682
BLAST score     723
E value        7.0e-77
Match length    139
% identity      99
NCBI Description (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No.        235488
Seq. ID         LIB3272-058-P1-K1-D3
Method          BLASTX
NCBI GI         g124224
BLAST score     682
E value        5.0e-72
Match length    135
% identity      95
NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
>gi_100345_pir_S21060 translation initiation factor eIF-5A
- common tobacco >gi_19887_emb_CAA45105_ (X63543)
eukaryotic initiation factor 5A (3) [Nicotiana tabacum]

Seq. No.        235489
Seq. ID         LIB3272-058-P1-K1-D4
Method          BLASTX
NCBI GI         g586797
BLAST score     236
E value        9.0e-20
Match length    100
% identity      44
NCBI Description HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III

Seq. No.        235490
Seq. ID         LIB3272-058-P1-K1-D5
Method          BLASTX
NCBI GI         g3023316
BLAST score     248
E value        4.0e-21
Match length    123
% identity      45
NCBI Description ALTERNATIVE OXIDASE 1 PRECURSOR >gi_558054_bbs_150257
(S71335) alternative oxidase, AOX [Nicotiana
tabacum=tobacco, cv Bright Yellow, suspension cells,
Peptide Mitochondrial, 353 aa] [Nicotiana tabacum]
>gi_1090812_prf_2019465A Aox1 gene [Nicotiana tabacum]

Seq. No.        235491
Seq. ID         LIB3272-058-P1-K1-D6
Method          BLASTX
NCBI GI         g1620898
BLAST score     581
E value        3.0e-60
Match length    141
% identity      81
NCBI Description (D87957) protein involved in sexual development [Homo
sapiens]

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Seq. No.      235503
Seq. ID       LIB3272-058-P1-K1-F10
Method        BLASTX
NCBI GI       g2995384
BLAST score    300
E value        2.0e-27
Match length   90
% identity     67
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
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Seq. No.      235505
Seq. ID      LIB3272-058-P1-K1-F12
Method       BLASTX
NCBI GI      g1666228
BLAST score   672
E value      7.0e-71
Match length  126
% identity    99
NCBI Description (U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin
[Pisum sativum] >gi_1724137 (U81046) actin [Pisum sativum]
>gi_1724139 (U81047) actin [Pisum sativum]
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34096

Seq. ID uC-gsflmaxxa001c12b1
 Method BLASTX
 NCBI GI g3355483
 BLAST score 298
 E value 4.0e-27
 Match length 59
 % identity 81
 NCBI Description (AC004218) gibberellin-regulated protein (GASA5)-like [Arabidopsis thaliana]

Seq. No. 235533
 Seq. ID uC-gsflmaxxa001d12b1
 Method BLASTX
 NCBI GI g2894558
 BLAST score 246
 E value 5.0e-21
 Match length 121
 % identity 60
 NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 235534
 Seq. ID uC-gsflmaxxa001f01b1
 Method BLASTX
 NCBI GI g1922246
 BLAST score 190
 E value 2.0e-14
 Match length 105
 % identity 42
 NCBI Description (Y10086) putative dehydrogenase [Arabidopsis thaliana]

Seq. No. 235535
 Seq. ID uC-gsflmaxxa001f05b1
 Method BLASTX
 NCBI GI g3402690
 BLAST score 153
 E value 3.0e-10
 Match length 101
 % identity 40
 NCBI Description (AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No. 235536
 Seq. ID uC-gsflmaxxa001f12b1
 Method BLASTX
 NCBI GI g3522937
 BLAST score 234
 E value 9.0e-20
 Match length 77
 % identity 61
 NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 235537
 Seq. ID uC-gsflmaxxa001h05b1
 Method BLASTX
 NCBI GI g3776015
 BLAST score 241
 E value 2.0e-20

Match length 110
 % identity 52
 NCBI Description (AJ010471) RNA helicase [Arabidopsis thaliana]
 >gi_4249378_gb_AAD14475_(AC005966) Identical to
 gb_AJ010471 mRNA for DEAD box RNA helicase (RH22) from
 Arabidopsis thaliana. EST gb_Y11191 comes from this gene.
 [Arabidopsis thaliana]

Seq. No. 235538
 Seq. ID uC-gsflmaxxa001h12b1
 Method BLASTX
 NCBI GI g4056457
 BLAST score 268
 E value 1.0e-23
 Match length 68
 % identity 75
 NCBI Description (AC005990) ESTs gb_234051 and gb_F13722 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 235539
 Seq. ID uC-gsflmaxxa002b04b1
 Method BLASTX
 NCBI GI g2213587
 BLAST score 301
 E value 1.0e-27
 Match length 107
 % identity 63
 NCBI Description (AC000348) T7N9.7 [Arabidopsis thaliana]

Seq. No. 235540
 Seq. ID uC-gsflmaxxa002b11b1
 Method BLASTX
 NCBI GI g2781345
 BLAST score 453
 E value 2.0e-45
 Match length 104
 % identity 78
 NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]

Seq. No. 235541
 Seq. ID uC-gsflmaxxa002d05b1
 Method BLASTX
 NCBI GI g4539420
 BLAST score 237
 E value 8.0e-20
 Match length 79
 % identity 62
 NCBI Description (AL049171) putative protein (fragment) [Arabidopsis
 thaliana]

Seq. No. 235542
 Seq. ID uC-gsflmaxxa002d06b1
 Method BLASTX
 NCBI GI g1449179
 BLAST score 334
 E value 3.0e-31
 Match length 116

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NCBI Description (AC000104) Similar to Nicotiana lesion-inducing ORF
(gb_U66269). [Arabidopsis thaliana]

Seq. No. 235559
Seq. ID uC-gsflmaxxa003e12b1
Method BLASTX
NCBI GI g2582665
BLAST score 499
E value 8.0e-51
Match length 105
% identity 94
NCBI Description (Z82983) thi [Citrus sinensis]

Seq. No. 235560
Seq. ID uC-gsflmaxxa003f01b1
Method BLASTX
NCBI GI g3452263
BLAST score 358
E value 3.0e-34
Match length 99
% identity 70
NCBI Description (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No. 235561
Seq. ID uC-gsflmaxxa003f02b1
Method BLASTX
NCBI GI g3738257
BLAST score 191
E value 1.0e-14
Match length 42
% identity 95
NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No. 235562
Seq. ID uC-gsflmaxxa003f03b1
Method BLASTX
NCBI GI g3892059
BLAST score 272
E value 5.0e-24
Match length 76
% identity 59
NCBI Description (AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 235563
Seq. ID uC-gsflmaxxa003f08b1
Method BLASTX
NCBI GI g3618343
BLAST score 369
E value 3.0e-35
Match length 148
% identity 47
NCBI Description (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]
>gi_4506223_ref_NP_002808.1_pPSMD13_proteasome (prosome, macropain) 26S subunit, non-ATPase,


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Seq. No.      235564
Seq. ID       uC-gsflmaxxa003g03b1
Method        BLASTX
NCBI GI       g4580388
BLAST score   224
E value       3.0e-18
Match length  130
% identity    43
NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]
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Seq. No.      235565
Seq. ID       uC-gsflmaxxa003g08b1
Method        BLASTX
NCBI GI       g4033424
BLAST score   363
E value       8.0e-35
Match length  82
% identity    87
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                  PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
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Seq. No.      235566
Seq. ID       uC-gsflmaxxa003g10b1
Method        BLASTX
NCBI GI       g3582002
BLAST score   153
E value       5.0e-10
Match length  94
% identity    40
NCBI Description (AJ010943) tomato invertase inhibitor [Lycopersicon
esculentum]
```

```
Seq. No.      235567
Seq. ID       uC-gsflmaxxa003h11b1
Method        BLASTX
NCBI GI       g4432839
BLAST score   355
E value       9.0e-34
Match length  78
% identity    46
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
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Seq. No.      235568
Seq. ID       uC-gsflmaxxa004d06b1
Method        BLASTX
NCBI GI       g4220524
BLAST score   180
E value       2.0e-13
Match length  40
% identity    78
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      235569
Seq. ID      uC-gsflmaxxa004e02b1
Method      BLASTX
```


Match length 85
 % identity 45
 NCBI Description PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM B
 >gi_1296666_emb_CAA65775_ (X97065) Sec23 protein [Homo sapiens]

Seq. No. 235575
 Seq. ID uC-gsflmaxxa004g09b1
 Method BLASTX
 NCBI GI g3236235
 BLAST score 317
 E value 3.0e-29
 Match length 93
 % identity 69
 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
 >gi_4056501 (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 235576
 Seq. ID uC-gsflmaxxa005a01b1
 Method BLASTX
 NCBI GI g2827718
 BLAST score 211
 E value 1.0e-16
 Match length 86
 % identity 56
 NCBI Description (AL021684) retrotransposon - like protein [Arabidopsis thaliana]

Seq. No. 235577
 Seq. ID uC-gsflmaxxa005b08b1
 Method BLASTX
 NCBI GI g3746063
 BLAST score 218
 E value 1.0e-17
 Match length 95
 % identity 43
 NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 235578
 Seq. ID uC-gsflmaxxa005b12b1
 Method BLASTX
 NCBI GI g4262229
 BLAST score 140
 E value 7.0e-09
 Match length 68
 % identity 44
 NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

Seq. No. 235579
 Seq. ID uC-gsflmaxxa005c03b1
 Method BLASTX
 NCBI GI g3702331
 BLAST score 269
 E value 1.0e-23
 Match length 139
 % identity 48

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235580
Seq. ID uC-gsflmaxxa005c05b1
Method BLASTX
NCBI GI g2842490
BLAST score 276
E value 6.0e-25
Match length 71
% identity 70

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 235581
Seq. ID uC-gsflmaxxa005d04b1
Method BLASTX
NCBI GI g3249095
BLAST score 230
E value 4.0e-19
Match length 69
% identity 67

NCBI Description (AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb_L13703 from Schizosaccharomyces pombe. ESTs gb_N37567 and gb_T43002 come from this gene. [Arabidopsis thaliana]

Seq. No. 235582
Seq. ID uC-gsflmaxxa005d08b1
Method BLASTX
NCBI GI g897638
BLAST score 278
E value 8.0e-25
Match length 56
% identity 96

NCBI Description (M10124) unknown protein [Nicotiana tabacum]
>gi_224349_prf__1102209C ORF 3 [Nicotiana sp.]

Seq. No. 235583
Seq. ID uC-gsflmaxxa006a04b1
Method BLASTX
NCBI GI g2880049
BLAST score 391
E value 4.0e-38
Match length 97
% identity 76

NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235584
Seq. ID uC-gsflmaxxa006a07b1
Method BLASTX
NCBI GI g4522012
BLAST score 406
E value 1.0e-39
Match length 111
% identity 70

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235585

Match length 67
 % identity 67
 NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine
 S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
 >gi_2129919_pir_S65957
 5-methyltetrahydropteroyltriglutamate--homocysteine
 S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
 >gi_886471_emb_CAA58474_ (X83499) methionine synthase
 [Catharanthus roseus]

Seq. No. 235591
 Seq. ID uC-gsflmaxxa009a12b1
 Method BLASTX
 NCBI GI g124712
 BLAST score 375
 E value 5.0e-36
 Match length 91
 % identity 73
 NCBI Description BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1 PRECURSOR
 (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) (CELL WALL
 BETA-FRUCTOSIDASE 1) >gi_100159_pir_JQ0991
 beta-fructofuranosidase (EC 3.2.1.26) precursor - carrot
 >gi_167551 (M58362). beta-fructosidase [Daucus carota]

Seq. No. 235592
 Seq. ID uC-gsflmaxxa009b09b1
 Method BLASTX
 NCBI GI g4263787
 BLAST score 212
 E value 5.0e-17
 Match length 92
 % identity 46
 NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]

Seq. No. 235593
 Seq. ID uC-gsflmaxxa009b12b1
 Method BLASTX
 NCBI GI g4455301
 BLAST score 243
 E value 9.0e-21
 Match length 71
 % identity 75
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 235594
 Seq. ID uC-gsflmaxxa009c04b1
 Method BLASTX
 NCBI GI g441457
 BLAST score 335
 E value 2.0e-31
 Match length 74
 % identity 88
 NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
 esculentum]

Seq. No. 235595
 Seq. ID uC-gsflmaxxa009c07b1

BLAST score 252
 E value 1.0e-21
 Match length 56
 % identity 86
 NCBI Description EUKARYOTIC INITIATION FACTOR 4A-15 (EIF-4A-15)
 >gi_485945_emb_CAA55739_ (X79138) NeIF-4A15 [Nicotiana
 tabacum]

Seq. No. 235601
 Seq. ID uC-gsflmaxxa009e08b1
 Method BLASTX
 NCBI GI g3822223
 BLAST score 309
 E value 6.0e-29
 Match length 70
 % identity 79
 NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1
 alpha subunit [Arabidopsis thaliana]

Seq. No. 235602
 Seq. ID uC-gsflmaxxa009f01b1
 Method BLASTX
 NCBI GI g2618686
 BLAST score 193
 E value 4.0e-15
 Match length 70
 % identity 47
 NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235603
 Seq. ID uC-gsflmaxxa009f03b1
 Method BLASTX
 NCBI GI g267075
 BLAST score 412
 E value 2.0e-40
 Match length 82
 % identity 89
 NCBI Description TUBULIN BETA-2 CHAIN >gi_388254_emb_CAA38614_ (X54845)
 beta-tubulin 2 [Pisum sativum]

Seq. No. 235604
 Seq. ID uC-gsflmaxxa009f06b1
 Method BLASTX
 NCBI GI g1419758
 BLAST score 357
 E value 2.0e-34
 Match length 75
 % identity 84
 NCBI Description (X98795) geranylgeranyl pyrophosphate synthase [Sinapis
 alba]

Seq. No. 235605
 Seq. ID uC-gsflmaxxa009f09b1
 Method BLASTX
 NCBI GI g2344887
 BLAST score 292
 E value 2.0e-26


```

Method                BLASTX
NCBI GI               g3540193
BLAST score           446
E value               2.0e-44
Match length          106
% identity             79
NCBI Description      (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.              235616
Seq. ID               uC-gsflmaxxa012a04b1
Method                BLASTX
NCBI GI               g1730566
BLAST score           497
E value               2.0e-50
Match length          141
% identity             69
NCBI Description      PHYTOCHROME E >gi_1145714 (U39787) phytochrome E [Ipomoea
nil]

Seq. No.              235617
Seq. ID               uC-gsflmaxxa012b04b1
Method                BLASTX
NCBI GI               g2315153
BLAST score           317
E value               2.0e-29
Match length          84
% identity             73
NCBI Description      (Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]

Seq. No.              235618
Seq. ID               uC-gsflmaxxa012b08b1
Method                BLASTX
NCBI GI               g3522939
BLAST score           210
E value               9.0e-17
Match length          68
% identity             60
NCBI Description      (AC004411) putative squamosa-promoter binding protein
[Arabidopsis thaliana]

Seq. No.              235619
Seq. ID               uC-gsflmaxxa012c04b1
Method                BLASTX
NCBI GI               g1621268
BLAST score           230
E value               3.0e-19
Match length          62
% identity             69
NCBI Description      (Z81012) unknown [Ricinus communis]

Seq. No.              235620
Seq. ID               uC-gsflmaxxa012d04b1
Method                BLASTX
NCBI GI               g3643607
BLAST score           354
E value               5.0e-34
Match length          81

```


retrovirus receptor [Rattus norvegicus]

```
Seq. No.      235626
Seq. ID       uC-gsflmaxxa015b07b1
Method        BLASTX
NCBI GI       g4335773
BLAST score    151
E value        8.0e-10
Match length   91
% identity     42
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      235627
Seq. ID      uC-gsflmaxxa015b09b1
Method       BLASTX
NCBI GI      g2623298
BLAST score   310
E value      2.0e-28
Match length  134
% identity    62
NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
thaliana]
```

```
Seq. No.      235628
Seq. ID       uC-gsflmaxxa015c03b1
Method        BLASTX
NCBI GI       g3080415
BLAST score   182
E value       6.0e-14
Match length  60
% identity    62
NCBI Description (AL022604) cysteine proteinase - like protein [Arabidopsis
                thaliana]
```

```
Seq. No.          235629
Seq. ID           uC-gsflmaxxa015f04b1
Method            BLASTX
NCBI GI           g130172
BLAST score       190
E value           6.0e-15
Match length      37
% identity        95
NCBI Description  ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH
                  PHOSPHORYLASE L) >gi_168276 (M64362) starch phosphorylase
                  [Ipomoea batatas]
```

```
Seq. No.          235630
Seq. ID           uC-gsflmaxxa015f11b1
Method            BLASTX
NCBI GI           g322641
BLAST score       322
E value           3.0e-30
Match length      86
% identity        63
NCBI Description  beta-1,3-glucanase homolog (clone A6) - rape (fragment)
                  >gi_17738_emb_CAA49513_(X69887) beta-1,3-glucanase
                  homologue [Brassica napus]
```


Seq. No. 235631
 Seq. ID uC-gsflmaxxa026a11b1
 Method BLASTX
 NCBI GI g4056507
 BLAST score 147
 E value 9.0e-10
 Match length 65
 % identity 54
 NCBI Description (AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No. 235632
 Seq. ID uC-gsflmaxxa026b01b1
 Method BLASTX
 NCBI GI g3080391
 BLAST score 238
 E value 4.0e-20
 Match length 75
 % identity 61
 NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 235633
 Seq. ID uC-gsflmaxxa026c01b1
 Method BLASTX
 NCBI GI g1652164
 BLAST score 333
 E value 3.0e-31
 Match length 111
 % identity 61
 NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 235634
 Seq. ID uC-gsflmaxxa026e03b1
 Method BLASTX
 NCBI GI g3150405
 BLAST score 208
 E value 8.0e-17
 Match length 82
 % identity 51
 NCBI Description (AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 235635
 Seq. ID uC-gsflmaxxa026f01b1
 Method BLASTX
 NCBI GI g2661412
 BLAST score 223
 E value 1.0e-18
 Match length 60
 % identity 75
 NCBI Description (AJ000728) MAP kinase kinase [Lycopersicon esculentum]

Seq. No. 235636
 Seq. ID uC-gsflmaxxa026g02b1
 Method BLASTX
 NCBI GI g3914826


```
Seq. No.      235647
Seq. ID       uC-gsflmaxxa027h03b1
Method        BLASTX
NCBI GI       g3513744
BLAST score    262
E value       6.0e-23
Match length   75
% identity     60
NCBI Description (AF080118) contains similarity to Medicago truncatula MtN3
                (GB:Y08726) [Arabidopsis thaliana]
```

```
Seq. No.      235648
Seq. ID       uC-gsflmaxxa027h04b1
Method        BLASTX
NCBI GI       g2738248
BLAST score   411
E value       3.0e-40
Match length  102
% identity    82
NCBI Description (U97200) cobalamin-independent methionine synthase
                [Arabidopsis thaliana]
```

```
Seq. No.      235649
Seq. ID      uC-gsflmaxxa027h12b1
Method       BLASTX
NCBI GI      g3036819
BLAST score   350
E value      3.0e-33
Match length  115
% identity    63
NCBI Description (AJ000058) MCM3 homolog [Arabidopsis thaliana]
```

```
Seq. No.      235650
Seq. ID      uC-gsflmaxxa028a07b1
Method       BLASTX
NCBI GI      g3522933
BLAST score   229
E value      6.0e-25
Match length  66
% identity    87
NCBI Description (AC004411) putative anion exchange protein 3 [Arabidopsis thaliana]
```

Seq. No.	235651
Seq. ID	uC-gsflmaxxa028a08b1
Method	BLASTX
NCBI GI	g4510426
BLAST score	312
E value	1.0e-28
Match length	128
% identity	54.
NCBI Description	(AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No.	235652
Seq. ID	uC-gsflmaxxa028b05b1
Method	BLASTX


```
Seq. No.      235657
Seq. ID       uC-gsflmaxxa028f12b1
Method        BLASTX
NCBI GI       g1502430
BLAST score   233
E value       9.0e-26
Match length  68
% identity    86
NCBI Description (U62331) phosphate transporter [Arabidopsis thaliana]
>gi_2564661 (AF022872) phosphate transporter [Arabidopsis
thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate
Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
phosphate transporter, AtPT2 [Arabidopsis thaliana]
```

Seq. No.	235658
Seq. ID	uC-gsflmaxxa028g03b1
Method	BLASTX
NCBI GI	g2244792
BLAST score	261
E value	1.0e-22
Match length	78
% identity	64
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

```
Seq. No.      235659
Seq. ID       uC-gsflmaxxa028g09b1
Method        BLASTX
NCBI GI       g4558664
BLAST score   191
E value       2.0e-14
Match length  72
% identity    28
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      235660
Seq. ID      uC-gsflmaxxa028h08b1
Method       BLASTX
NCBI GI      g2154715
BLAST score   321
E value      1.0e-42
Match length  96
% identity    92
NCBI Description (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
```

```
Seq. No.      235661
Seq. ID      uC-gsflmaxxa029b01b1
Method       BLASTX
NCBI GI      g1130684
BLAST score   429
E value      1.0e-42
Match length  88
% identity    95
NCBI Description (Z46960) acetohydroxyacid synthase [Gossypium hirsutum]
```

```
Seq. No.      235662
Seq. ID      uC-gsflmaxxa029b10b1
Method      BLASTX
```


NCBI GI g3297824
 BLAST score 161
 E value 3.0e-11
 Match length 82
 % identity 49
 NCBI Description (AL031032) bZIP transcription factor - like protein
 [Arabidopsis thaliana]

Seq. No. 235663
 Seq. ID uC-gsflmaxxa029d09b1
 Method BLASTX
 NCBI GI g3128228
 BLAST score 337
 E value 7.0e-32
 Match length 72
 % identity 89
 NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis
 thaliana] >gi_3337376 (AC004481) putative ribosomal protein
 L18A [Arabidopsis thaliana]

Seq. No. 235664
 Seq. ID uC-gsflmaxxa029d10b1
 Method BLASTX
 NCBI GI g2495256
 BLAST score 564
 E value 3.0e-58
 Match length 121
 % identity 89
 NCBI Description STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG
 PROTEIN) >gi_481756_pir_S39242 HMG protein - Madagascar
 periwinkle >gi_433872_emb_CAA82251_ (Z28410) HMG protein
 [Catharanthus roseus]

Seq. No. 235665
 Seq. ID uC-gsflmaxxa029e03b1
 Method BLASTX
 NCBI GI g2760836
 BLAST score 291
 E value 1.0e-26
 Match length 90
 % identity 68
 NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis
 thaliana]

Seq. No. 235666
 Seq. ID uC-gsflmaxxa029e06b1
 Method BLASTX
 NCBI GI g1171642
 BLAST score 187
 E value 1.0e-14
 Match length 45
 % identity 80
 NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
 >gi_481206_pir_S38326 protein kinase - Arabidopsis
 thaliana >gi_166809 (L07248) protein kinase [Arabidopsis
 thaliana]

Seq. No. 235667
 Seq. ID uC-gsflmaxxa029e07b1
 Method BLASTX
 NCBI GI g1843527
 BLAST score 182
 E value 5.0e-14
 Match length 42
 % identity 90
 NCBI Description (U73747) annexin [*Gossypium hirsutum*]

Seq. No. 235668
 Seq. ID uC-gsflmaxxa029f04b1
 Method BLASTX
 NCBI GI g3738338
 BLAST score 282
 E value 3.0e-25
 Match length 113
 % identity 50
 NCBI Description (AC005170) putative polygalacturonase [*Arabidopsis thaliana*]

Seq. No. 235669
 Seq. ID uC-gsflmaxxa029f10b1
 Method BLASTX
 NCBI GI g2911075
 BLAST score 397
 E value 8.0e-39
 Match length 110
 % identity 70
 NCBI Description (A1021960) putative protein [*Arabidopsis thaliana*]

Seq. No. 235670
 Seq. ID uC-gsflmaxxa029f12b1
 Method BLASTX
 NCBI GI g544426
 BLAST score 231
 E value 4.0e-19
 Match length 85
 % identity 81
 NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN >gi_100155_pir_S14857
 glycine-rich protein - carrot >gi_18347_emb_CAA41152_
 (X58146) glycine-rich protein [*Daucus carota*]
 >gi_445138_prf_1908438A Gly-rich protein [*Daucus carota*]

Seq. No. 235671
 Seq. ID uC-gsflmaxxa029h01b1
 Method BLASTX
 NCBI GI g3860323
 BLAST score 158
 E value 1.0e-10
 Match length 38
 % identity 82
 NCBI Description (AJ012688) hypothetical protein [*Cicer arietinum*]

Seq. No. 235672
 Seq. ID uC-gsflmaxxa029h05b1
 Method BLASTX

NCBI Description (297336) CCAAT-binding transcription factor subunit
A(CBF-A) [Arabidopsis thaliana]

Seq. No. 235704
Seq. ID uC-gsflmaxxa040e07b1
Method BLASTX
NCBI GI g3183445
BLAST score 299
E value 4.0e-27
Match length 140
% identity 46

NCBI Description HYPOTHETICAL 30.8 KD PROTEIN IN PPHB-RPOS INTERGENIC REGION
>gi_882629 (U29579) ORF_o302 [Escherichia coli] >gi_1789092
(AE000357) putative dehydrogenase [Escherichia coli]

Seq. No. 235705
Seq. ID uC-gsflmaxxa040e09b1
Method BLASTX
NCBI GI g3056595
BLAST score 247
E value 3.0e-21
Match length 103
% identity 50

NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]

Seq. No. 235706
Seq. ID uC-gsflmaxxa040f01b1
Method BLASTX
NCBI GI g3892059
BLAST score 529
E value 5.0e-54
Match length 146
% identity 71

NCBI Description (AC002330) predicted protein of unknown function
[Arabidopsis thaliana]

Seq. No. 235707
Seq. ID uC-gsflmaxxa040f05b1
Method BLASTX
NCBI GI g2191175
BLAST score 450
E value 8.0e-45
Match length 141
% identity 61

NCBI Description (AF007270) A_IG002P16.24 gene product [Arabidopsis
thaliana]

Seq. No. 235708
Seq. ID uC-gsflmaxxa040g09b1
Method BLASTX
NCBI GI g3881189
BLAST score 419
E value 3.0e-41
Match length 96
% identity 77

NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST
EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337

0903401610100

```
Seq. No.      235713
Seq. ID       uC-gsflmaxxa041a09b1
Method        BLASTX
NCBI GI       g1707032
BLAST score   305
E value       7.0e-28
Match length  126
% identity    32
NCBI Description (U80445) coded for by C. elegans cDNA yk13g5.3; coded for
                by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA
                CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for
```


09634013-101000

34140

E value 4.0e-27
 Match length 108
 % identity 56
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
 >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 235741
 Seq. ID uC-gsflmaxxa043b07b1
 Method BLASTX
 NCBI GI g4455293
 BLAST score 248
 E value 2.0e-21
 Match length 68
 % identity 74
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 235742
 Seq. ID uC-gsflmaxxa043b09b1
 Method BLASTX
 NCBI GI g557474
 BLAST score 154
 E value 4.0e-10
 Match length 99
 % identity 35
 NCBI Description (U15179) ORF1 [Bacteroides ovatus]

Seq. No. 235743
 Seq. ID uC-gsflmaxxa043e10b1
 Method BLASTX
 NCBI GI g4432835
 BLAST score 200
 E value 1.0e-15
 Match length 83
 % identity 45
 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 235744
 Seq. ID uC-gsflmaxxa043f02b1
 Method BLASTX
 NCBI GI g2623298
 BLAST score 323
 E value 7.0e-30
 Match length 75
 % identity 76
 NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No. 235745
 Seq. ID uC-gsflmaxxa043f07b1
 Method BLASTX
 NCBI GI g2760830
 BLAST score 228
 E value 8.0e-19
 Match length 99
 % identity 45
 NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

03684019-101000

```
Seq. No.      235747
Seq. ID      uC-gsflmaxxa043h07b1
Method       BLASTX
NCBI GI      g4406777
BLAST score   184
E value      3.0e-14
Match length  37
% identity    92
NCBI Description (AC006532) putative zinc-finger protein [Arabidopsis thaliana]
```

```
Seq. No.      235749
Seq. ID       uC-gsflmaxxa045d05b1
Method        BLASTX
NCBI GI       g2505870
BLAST score   604
E value       7.0e-63
Match length  138
% identity    86
NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	235751
Seq. ID	uC-gsflmaxxa045e12b1

Match length 92
 % identity 79
 NCBI Description (Y10116) signal recognition particle subunit 14
 [Arabidopsis thaliana]

Seq. No. 235777
 Seq. ID uC-gsflmaxxa047c10b1
 Method BLASTX
 NCBI GI g4544445
 BLAST score 617
 E value 2.0e-64
 Match length 148
 % identity 82
 NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate
 1-phosphotransferase [Arabidopsis thaliana]

Seq. No. 235778
 Seq. ID uC-gsflmaxxa047e03b1
 Method BLASTX
 NCBI GI g4469023
 BLAST score 560
 E value 1.0e-57
 Match length 128
 % identity 83
 NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 235779
 Seq. ID uC-gsflmaxxa047e06b1
 Method BLASTX
 NCBI GI g3935152
 BLAST score 237
 E value 5.0e-20
 Match length 55
 % identity 80
 NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No. 235780
 Seq. ID uC-gsflmaxxa047f04b1
 Method BLASTX
 NCBI GI g4335731
 BLAST score 160
 E value 8.0e-11
 Match length 126
 % identity 31
 NCBI Description (AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No. 235781
 Seq. ID uC-gsflmaxxa047f05b1
 Method BLASTX
 NCBI GI g3062801
 BLAST score 477
 E value 4.0e-48
 Match length 120
 % identity 75
 NCBI Description (AB012873) arginine decarboxylase [Nicotiana sylvestris]

Seq. No. 235782

Method BLASTX
 NCBI GI g3885338
 BLAST score 179
 E value 6.0e-13
 Match length 80
 % identity 39
 NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 235793
 Seq. ID uC-gsflmaxxa048e05b1
 Method BLASTX
 NCBI GI g3098603
 BLAST score 175
 E value 2.0e-12
 Match length 111
 % identity 33
 NCBI Description (AF052191) katanin p60 subunit [Strongylocentrotus purpuratus]

Seq. No. 235794
 Seq. ID uC-gsflmaxxa048e07b1
 Method BLASTX
 NCBI GI g1621268
 BLAST score 221
 E value 4.0e-18
 Match length 60
 % identity 70
 NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 235795
 Seq. ID uC-gsflmaxxa048f06b1
 Method BLASTX
 NCBI GI g4038030
 BLAST score 382
 E value 8.0e-37
 Match length 151
 % identity 50
 NCBI Description (AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No. 235796
 Seq. ID uC-gsflmaxxa048f11b1
 Method BLASTX
 NCBI GI g2065531
 BLAST score 320
 E value 7.0e-30
 Match length 60
 % identity 92
 NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 235797
 Seq. ID uC-gsflmaxxa048g05b1
 Method BLASTX
 NCBI GI g4158232
 BLAST score 581
 E value 4.0e-60
 Match length 128

% identity 88
 NCBI Description (Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No. 235798
 Seq. ID uC-gsflmaxxa048g07b1
 Method BLASTX
 NCBI GI g2760320
 BLAST score 332
 E value 6.0e-31
 Match length 130
 % identity 52
 NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No. 235799
 Seq. ID uC-gsflmaxxa048h03b1
 Method BLASTX
 NCBI GI g2739374
 BLAST score 457
 E value 1.0e-45
 Match length 141
 % identity 32
 NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235800
 Seq. ID uC-gsflmaxxa048h05b1
 Method BLASTX
 NCBI GI g2147966
 BLAST score 239
 E value 5.0e-20
 Match length 82
 % identity 57
 NCBI Description probable 1-acyl-sn-glycerol-3-phosphate acyltransferase - Limnanthes douglasii >gi_1067138_emb_CAA88620_ (Z48730)
 1-acyl-sn-glycerol-3-phosphate acyltransferase (putative) [Limnanthes douglasii]

Seq. No. 235801
 Seq. ID uC-gsflmaxxa048h08b1
 Method BLASTX
 NCBI GI g586004
 BLAST score 251
 E value 9.0e-22
 Match length 53
 % identity 91
 NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir_S34267
 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_542090_pir_S40404 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139)
 superoxide dismutase [Ipomoea batatas]

Seq. No. 235802
 Seq. ID uC-gsflmaxxa049a02b1
 Method BLASTX
 NCBI GI g1076668
 BLAST score 183
 E value 1.0e-13

Seq. No. 235818
 Seq. ID uC-gsflmaxxa054a08b1
 Method BLASTX
 NCBI GI g3386614
 BLAST score 247
 E value 3.0e-21
 Match length 58
 % identity 35
 NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No. 235819
 Seq. ID uC-gsflmaxxa054a12b1
 Method BLASTX
 NCBI GI g4455202
 BLAST score 261
 E value 7.0e-23
 Match length 65
 % identity 77
 NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 235820
 Seq. ID uC-gsflmaxxa054b12b1
 Method BLASTX
 NCBI GI g3688189
 BLAST score 382
 E value 3.0e-37
 Match length 92
 % identity 80
 NCBI Description (AL031804) putative protein kinase [Arabidopsis thaliana]

Seq. No. 235821
 Seq. ID uC-gsflmaxxa054c02b1
 Method BLASTX
 NCBI GI g128592
 BLAST score 383
 E value 6.0e-37
 Match length 99
 % identity 71
 NCBI Description POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
 >gi_82190_pir_S22495 pollen-specific protein precursor -
 common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
 specific protein [Nicotiana tabacum]

Seq. No. 235822
 Seq. ID uC-gsflmaxxa054c10b1
 Method BLASTX
 NCBI GI g2832625
 BLAST score 230
 E value 3.0e-19
 Match length 97
 % identity 52
 NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 235823
 Seq. ID uC-gsflmaxxa054e05b1

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% identity      80
NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis
thaliana]

Seq. No.       235855
Seq. ID        uC-gsflmaxxa058a09b1
Method         BLASTX
NCBI GI        g3355486
BLAST score    367
E value        4.0e-35
Match length   97
% identity     68
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.       235856
Seq. ID        uC-gsflmaxxa058b04b1
Method         BLASTX
NCBI GI        g2497953
BLAST score    361
E value        1.0e-34
Match length   98
% identity     73
NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM
COFACTOR BIOSYNTHESIS ENZYME CNX1). >gi_1263314 (L47323)
molybdenum cofactor biosynthesis enzyme [Arabidopsis
thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum
cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.       235857
Seq. ID        uC-gsflmaxxa058b10b1
Method         BLASTX
NCBI GI        g4185139
BLAST score    299
E value        2.0e-27
Match length   93
% identity     62
NCBI Description (AC005724) putative diacylglycerol kinase [Arabidopsis
thaliana]

Seq. No.       235858
Seq. ID        uC-gsflmaxxa058c02b1
Method         BLASTX
NCBI GI        g3169178
BLAST score    199
E value        2.0e-15
Match length   59
% identity     63
NCBI Description (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.       235859
Seq. ID        uC-gsflmaxxa058c03b1
Method         BLASTX
NCBI GI        g2501449
BLAST score    245
E value        1.0e-20
Match length   53

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```
Seq. No.      235866
Seq. ID       uC-gsflmaxxa058g07b1
Method        BLASTX
NCBI GI       g1663722
BLAST score   386
E value       2.0e-37
Match length  133
% identity    53
NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
```

```
Seq. No.      235868
Seq. ID       uC-gsflmaxxa058h10b1
Method        BLASTX
NCBI GI       g2244752
BLAST score   194
E value       7.0e-15
Match length  108
% identity    39
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	235869
Seq. ID	uC-gsflmaxxa060a04b1
Method	BLASTX
NCBI GI	g4103152
BLAST score	165
E value	5.0e-12
Match length	59
% identity	56
NCBI Description	(AF020716) histidyl-tRNA synthetase [Triticum aestivum]

34166


```
Seq. No.      235876
Seq. ID       uC-gsflmaxxa060f11b1
Method        BLASTX
NCBI GI       g2459415
BLAST score   146
E value       3.0e-09
Match length  83
% identity    43
NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]
```

Seq. No.	235877
Seq. ID	uC-gsflmaxxa060g02b1
Method	BLASTX
NCBI GI	g3033393
BLAST score	234
E value	1.0e-19
Match length	66
% identity	70
NCBI Description	(AC004238) putative phosphatidylinositol-glycan-class C (PIGC) [<i>Arabidopsis thaliana</i>]

```
Seq. No.      235878
Seq. ID       uC-gsflmaxxa061a02b1
Method        BLASTX
NCBI GI       g2146735
BLAST score   556
E value       2.0e-57
Match length  114
% identity    92
NCBI Description  glucose-6-phosphate 1-dehydrogenase (EC 1:1.1.49) (clone
E5) - Arabidopsis thaliana (fragment)
>gi_1166405_emb_CAA59011_(X84229) glucose-6-phosphate
1-dehydrogenase [Arabidopsis thaliana]
```

```
Seq. No.      235879
Seq. ID       uC-gsflmaxxa061a09b1
Method        BLASTX
NCBI GI       g2501182
BLAST score   587
E value       7.0e-61
Match length  147
% identity    72
NCBI Description OSMOTIN-LIKE PROTEIN PRECURSOR >gi_2129934_pir_JC5237
osmotin-like protein - tomato >gi_1220537 (L76632)
osmotin-like protein [Lycopersicon esculentum]
```

```
Seq. No.      235880
Seq. ID       uC-gsflmaxxa061a11b1
Method        BLASTX
NCBI GI       g4510383
BLAST score   223
E value       3.0e-18
Match length  69
% identity    70
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
```

Seq. No. 235881

Seq. ID uC-gsflmaxxa061b01b1
 Method BLASTX
 NCBI GI g585452
 BLAST score 601
 E value 5.0e-65
 Match length 134
 % identity 90
 NCBI Description MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM
 PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)
 (NAD-ME) >gi_1076666_pir_A53318 malate dehydrogenase
 (decarboxylating) (EC 1.1.1.39) 59K chain precursor,
 mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002)
 precursor of the 59kDa subunit of the mitochondrial
 NAD+-dependent malic enzyme [Solanum tuberosum]

Seq. No. 235882
 Seq. ID uC-gsflmaxxa061b04b1
 Method BLASTX
 NCBI GI g4467110
 BLAST score 224
 E value 2.0e-18
 Match length 114
 % identity 36
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 235883
 Seq. ID uC-gsflmaxxa061b08b1
 Method BLASTX
 NCBI GI g2547036
 BLAST score 193
 E value 1.0e-14
 Match length 90
 % identity 53
 NCBI Description (Y13920) ribosomal protein S2 [Triticum aestivum]

Seq. No. 235884
 Seq. ID uC-gsflmaxxa061b12b1
 Method BLASTX
 NCBI GI g1495366
 BLAST score 394
 E value 3.0e-38
 Match length 104
 % identity 69
 NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 235885
 Seq. ID uC-gsflmaxxa061c06b1
 Method BLASTX
 NCBI GI g4249410
 BLAST score 148
 E value 3.0e-09
 Match length 99
 % identity 49
 NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 235886
 Seq. ID uC-gsflmaxxa061d03b1

Method BLASTX
 NCBI GI g1169451
 BLAST score 441
 E value 7.0e-44
 Match length 125
 % identity 66
 NCBI Description PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR
 ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
 (BETA-1,3-ENDOGLUCANASE) >gi_322510_pir_S31906
 beta-1,3-glucanase homolog - Arabidopsis thaliana
 >gi_22677_emb_CAA49853_(X70409) A6 [Arabidopsis thaliana]
 >gi_2244764_emb_CAB10187_(Z97335) AMP-binding protein
 [Arabidopsis thaliana]

Seq. No. 235912
 Seq. ID uC-gsflmaxxa070c06b1
 Method BLASTX
 NCBI GI g2129944
 BLAST score 331
 E value 4.0e-31
 Match length 88
 % identity 68
 NCBI Description RNA-binding protein RZ-1 - wood tobacco
 >gi_1395193_dbj_BAA12064_(D83696) RNA-binding protein RZ-1
 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_(D28861)
 RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No. 235913
 Seq. ID uC-gsflmaxxa070c11b1
 Method BLASTX
 NCBI GI g3292827
 BLAST score 234
 E value 1.0e-19
 Match length 51
 % identity 82
 NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 235914
 Seq. ID uC-gsflmaxxa070e03b1
 Method BLASTX
 NCBI GI g3256068
 BLAST score 164
 E value 3.0e-23
 Match length 109
 % identity 50
 NCBI Description (Y14068) Heat Shock Factor 3 [Arabidopsis thaliana]

Seq. No. 235915
 Seq. ID uC-gsflmaxxa070g12b1
 Method BLASTX
 NCBI GI g3790587
 BLAST score 400
 E value 4.0e-39
 Match length 99
 % identity 73
 NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
 thaliana]

esculentum]

Seq. No. 235926
 Seq. ID uC-gsflmaxxa076c05b1
 Method BLASTX
 NCBI GI g2914703
 BLAST score 265
 E value 4.0e-23
 Match length 101
 % identity 28
 NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 235927
 Seq. ID uC-gsflmaxxa076c11b1
 Method BLASTX
 NCBI GI g2493895
 BLAST score 484
 E value 8.0e-49
 Match length 119
 % identity 77
 NCBI Description CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE)
 (O-ACETYL SERINE (THIOL)-LYASE) (CSASE)
 >gi_1071911_pir_S46438 cysteine synthase (EC 4.2.99.8) -
 watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine
 synthase [Citrullus lanatus]

Seq. No. 235928
 Seq. ID uC-gsflmaxxa076d03b1
 Method BLASTX
 NCBI GI g134891
 BLAST score 184
 E value 1.0e-13
 Match length 99
 % identity 42
 NCBI Description SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
 (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
 >gi_89066_pir_A24570 signal recognition particle receptor
 precursor - dog >gi_997_emb_CAA26945_ (X03184) signal
 recognition particle receptor [Canis sp.]
 >gi_224778_prf_1112224A signal recognition particle
 receptor [Canis familiaris]

Seq. No. 235929
 Seq. ID uC-gsflmaxxa076d05b1
 Method BLASTX
 NCBI GI g3582344
 BLAST score 213
 E value 5.0e-17
 Match length 117
 % identity 50
 NCBI Description (AC005496) putative cell division protein [Arabidopsis
 thaliana]

Seq. No. 235930
 Seq. ID uC-gsflmaxxa076e09b1
 Method BLASTX
 NCBI GI g2642428

Seq. No. 235936
 Seq. ID uC-gsflmaxxa088b09b1
 Method BLASTX
 NCBI GI g2244956
 BLAST score 220
 E value 5.0e-18
 Match length 133
 % identity 38
 NCBI Description (Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No. 235937
 Seq. ID uC-gsflmaxxa088b10b1
 Method BLASTX
 NCBI GI g3367515
 BLAST score 279
 E value 8.0e-25
 Match length 97
 % identity 56
 NCBI Description (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb_AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 235938
 Seq. ID uC-gsflmaxxa088c07b1
 Method BLASTX
 NCBI GI g3928084
 BLAST score 485
 E value 7.0e-49
 Match length 148
 % identity 66
 NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No. 235939
 Seq. ID uC-gsflmaxxa088d12b1
 Method BLASTX
 NCBI GI g2832649
 BLAST score 392
 E value 7.0e-38
 Match length 95
 % identity 79
 NCBI Description (AL021710) adenylosuccinate lyase - like protein [Arabidopsis thaliana]

Seq. No. 235940
 Seq. ID uC-gsflmaxxa088e08b1
 Method BLASTX
 NCBI GI g3641252
 BLAST score 404
 E value 1.0e-39
 Match length 111
 % identity 72
 NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Match length 38
 % identity 79
 NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
 >gi_485498_pir_S33533·heat shock protein 90 homolog
 precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
 homologue [Hordeum vulgare]

Seq. No. 235952
 Seq. ID uC-gsflmaxxa089h11b1
 Method BLASTX
 NCBI GI g2344901
 BLAST score 724
 E value 7.0e-77
 Match length 164
 % identity 82
 NCBI Description (AC002388) serine/threonine protein kinase isolog
 [Arabidopsis thaliana]

Seq. No. 235953
 Seq. ID uC-gsflmaxxa090a06b1
 Method BLASTX
 NCBI GI g2982311
 BLAST score 200
 E value 5.0e-16
 Match length 49
 % identity 78
 NCBI Description (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
 mariana]

Seq. No. 235954
 Seq. ID uC-gsflmaxxa090c04b1
 Method BLASTX
 NCBI GI g3522942
 BLAST score 575
 E value 2.0e-59
 Match length 155
 % identity 66
 NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235955
 Seq. ID uC-gsflmaxxa090c06b1
 Method BLASTX
 NCBI GI g421955
 BLAST score 515
 E value 6.0e-59
 Match length 160
 % identity 65
 NCBI Description hypothetical protein 4 - potato transposon Tst1
 >gi_21434_emb_CAA36616_ (X52387) ORF4 [Solanum tuberosum]

Seq. No. 235956
 Seq. ID uC-gsflmaxxa090c11b1
 Method BLASTX
 NCBI GI g2529677
 BLAST score 492
 E value 6.0e-50
 Match length 115

NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235968
Seq. ID uC-gsflmaxxa091f04b1
Method BLASTX
NCBI GI g1872521
BLAST score 191
E value 2.0e-14

Match length 51
% identity 25
NCBI Description (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
>gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No. 235969
Seq. ID uC-gsflmaxxa091g01b1
Method BLASTX
NCBI GI g416664
BLAST score 388
E value 1.0e-37
Match length 113
% identity 68

NCBI Description PLASMA MEMBRANE ATPASE 4 (PROTON PUMP)
>gi_485504_pir_S33548 H+-transporting ATPase (EC 3.6.1.35)
type 4, plasma membrane - curled-leaved tobacco
>gi_19704_emb_CAA47275 (X66737) plasma membrane H+-ATPase
[Nicotiana glauca]

Seq. No. 235970
Seq. ID uC-gsflmaxxa091g03b1
Method BLASTX
NCBI GI g1621012
BLAST score 642
E value 2.0e-67
Match length 134
% identity 90

NCBI Description (Y08786) 1,4-alpha-glucan branching enzyme [Solanum tuberosum]

Seq. No. 235971
Seq. ID uC-gsflmaxxa091g05b1
Method BLASTX
NCBI GI g4454471
BLAST score 145
E value 4.0e-09
Match length 58
% identity 55

NCBI Description (AC006234) putative G protein coupled receptor [Arabidopsis thaliana]

Seq. No. 235972
Seq. ID uC-gsflmaxxa091g07b1
Method BLASTX
NCBI GI g3608485
BLAST score 439
E value 2.0e-43
Match length 87


```
%identity          94
NCBI Description   (AF088915)  proteasome beta subunit [Petunia x hybrida]

Seq. No.          235973
Seq. ID           uC-gsflmaxxa091g11b1
Method            BLASTX
NCBI GI           g1076663
BLAST score       262
E value           8.0e-23
Match length      54
% identity        96
NCBI Description   H+-transporting ATPase (EC 3.6.1.35) (clone PHA2) - potato
>gi_435001_emb_CAA54045_ (X76535) H(+)-transporting ATPase
[Solanum tuberosum]
```

Seq. No.	235974
Seq. ID	uC-gsflmaxxa091h08b1
Method	BLASTX
NCBI GI	g3135693
BLAST score	379
E value	2.0e-36
Match length	74
% identity	97
NCBI Description	(AF064201) glutathione S-transferase [Gossypium hirsutum]

```
Seq. No.      235975
Seq. ID      uC-gsflmaxxa091h11b1
Method       BLASTX
NCBI GI      g2160692
BLAST score   513
E value      3.0e-52
Match length  125
% identity    72
NCBI Description (U73527) B' regulatory subunit of PP2A [Arabidopsis
                thaliana]
```

```
Seq. No.      235976
Seq. ID       uC-gsflmaxxa092a06b1
Method        BLASTX
NCBI GI       g2651302
BLAST score    220
E value       3.0e-18
Match length   77
% identity     52
NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      235977
Seq. ID       uC-gsflmaxxa092c05b1
Method        BLASTX
NCBI GI       g4263821
BLAST score    390
E value        7.0e-38
Match length   122
% identity     70
NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 235978

Seq. ID uC-gsflmaxxa092g07b1
 Method BLASTX
 NCBI GI g220838
 BLAST score 169
 E value 3.0e-12
 Match length 55
 % identity 56
 NCBI Description (D10655) dihydrolipoamide acetyltransferase [Rattus rattus]

Seq. No. 235979
 Seq. ID uC-gsflmaxxa092h07b1
 Method BLASTX
 NCBI GI g1708236
 BLAST score 157
 E value 3.0e-24
 Match length 83
 % identity 62
 NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
 (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
 >gi_2129617_pir_JC4567 hydroxymethylglutaryl-CoA synthase
 (EC 4.1.3.5) - Arabidopsis thaliana
 >gi_1143390_emb_CAA58763_ (X83882)
 hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
 >gi_1586548_prf_2204245A hydroxy methylglutaryl CoA
 synthase [Arabidopsis thaliana]

Seq. No. 235980
 Seq. ID uC-gsflmaxxa092h08b1
 Method BLASTX
 NCBI GI g1666234
 BLAST score 169
 E value 2.0e-22
 Match length 61
 % identity 93
 NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin
 [Pisum sativum]

Seq. No. 235981
 Seq. ID uC-gsflmaxxa093h08b1
 Method BLASTX
 NCBI GI g4467096
 BLAST score 189
 E value 2.0e-14
 Match length 106
 % identity 42
 NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 235982
 Seq. ID uC-gsflmaxxa094b01b1
 Method BLASTX
 NCBI GI g1335862
 BLAST score 165
 E value 5.0e-12
 Match length 35
 % identity 91
 NCBI Description (U42608) clathrin heavy chain [Glycine max]

E value 1.0e-57
 Match length 123
 % identity 82
 NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 235994
 Seq. ID uC-gsflmaxxa096a08b1
 Method BLASTX
 NCBI GI g2980791
 BLAST score 554
 E value 5.0e-57
 Match length 121
 % identity 86
 NCBI Description (AL022197) actin depolymerizing factor - like protein [Arabidopsis thaliana]

Seq. No. 235995
 Seq. ID uC-gsflmaxxa096a12b1
 Method BLASTX
 NCBI GI g4512683
 BLAST score 402
 E value 3.0e-39
 Match length 96
 % identity 77
 NCBI Description (AC006931) putative lipase [Arabidopsis thaliana]
 >gi_4559323_gb_AAD22985.1_AC007087_4 (AC007087) putative
 lipase [Arabidopsis thaliana]

Seq. No. 235996
 Seq. ID uC-gsflmaxxa096b04b1
 Method BLASTX
 NCBI GI g1174469
 BLAST score 173
 E value 2.0e-12
 Match length 51
 % identity 61
 NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
 (INTEGRAL MEMBRANE PROTEIN 1) >gi_624704 (L38961) putative
 transmembrane protein precursor [Homo sapiens]
 >gi_1588286_prf_2208301B integral membrane protein [Homo
 sapiens] >gi_4504787_ref_NP_002210.1_pITM1_ integral
 transmembrane protein

Seq. No. 235997
 Seq. ID uC-gsflmaxxa096c07b1
 Method BLASTX
 NCBI GI g3047108
 BLAST score 157
 E value 2.0e-10
 Match length 130
 % identity 38
 NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 235998
 Seq. ID uC-gsflmaxxa096d10b1
 Method BLASTX
 NCBI GI g508304


```
Seq. No.      236004
Seq. ID      uC-gsflmaxxa096h01b1
Method       BLASTX
NCBI GI      g2244799
BLAST score   196
E value      3.0e-15
Match length  98
% identity    46
NCBI Description (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
```

```
Seq. No.      236005
Seq. ID      uC-gsflmaxxa096h04b1
Method       BLASTX
NCBI GI      g1483177
BLAST score   324
E value      6.0e-30
Match length  141
% identity    45
NCBI Description (D86598) antifreeze-like protein (af70) [Picea abies]
```

```
Seq. No.          236006
Seq. ID           uC-gsflmaxxa097b10b1
Method            BLASTX
NCBI GI           g4063751
BLAST score       323
E value           6.0e-30
Match length      138
% identity        54
NCBI Description   (AC005851) putative white protein [Arabidopsis thaliana]
                   >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                   protein [Arabidopsis thaliana]
```

Seq. No.	236007
Seq. ID	uC-gsflmaxxa097b12b1
Method	BLASTX
NCBI GI	g2708745
BLAST score	544
E value	6.0e-56
Match length	120
% identity	86
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

```
Seq. No.      236008
Seq. ID      uC-gsflmaxxa097c11b1
Method       BLASTX
NCBI GI      g1707032
BLAST score   148
E value      1.0e-09
Match length  83
% identity    43
NCBI Description (U80445) coded for by C. elegans cDNA yk13g5.3; coded for
by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA
CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for
by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA
yk65h8
```


090913-1030

```
Seq. No.          236015
Seq. ID           uC-gsflmaxxa097h06b1
Method            BLASTX
NCBI GI           g3228517
BLAST score       429
E value           2.0e-42
Match length      133
% identity        63
NCBI Description   (AF007788) ETTIN [Arabidopsis thaliana]
```

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Seq. No.      236017
Seq. ID      uC-gsflmaxxa098b02b1
Method       BLASTX
NCBI GI      g3763917
BLAST score   452
E value      6.0e-45
Match length  129
% identity    71
NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]
               >gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224)
               hypothetical protein [Arabidopsis thaliana]
```

34195

Seq. No.	236019
Seq. ID	uC-gsflmaxxa098b11b1
Method	BLASTX
NCBI GI	g82306
BLAST score	605
E value	7.0e-63
Match length	127
% identity	87
NCBI Description	myb protein 305 - garden snapdragon
Seq. No.	236020
Seq. ID	uC-gsflmaxxa098b12b1
Method	BLASTX
NCBI GI	g4538926
BLAST score	276
E value	2.0e-24
Match length	94
% identity	56
NCBI Description	(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]
Seq. No.	236021
Seq. ID	uC-gsflmaxxa098c07b1
Method	BLASTX
NCBI GI	g2511693
BLAST score	270
E value	1.0e-23
Match length	71
% identity	73
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.	236022
Seq. ID	uC-gsflmaxxa098c11b1
Method	BLASTX
NCBI GI	g120672
BLAST score	722
E value	1.0e-76
Match length	162
% identity	87
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66016_pir_DEPZG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - parsley >gi_20549_emb_CAA42902_ (X60344) glyceraldehyde 3-phosphate dehydrogenase [Petroselinum crispum]
Seq. No.	236023
Seq. ID	uC-gsflmaxxa098d04b1
Method	BLASTX
NCBI GI	g1168537
BLAST score	338
E value	1.0e-31
Match length	132
% identity	51
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir_JS0732 aspartic proteinase (EC 3.4.23.-) - rice >gi_218143_dbj_BAA02242_ (D12777)..aspartic proteinase

096415 101000

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Seq. No.      236025
Seq. ID       uC-gsflmaxxa098f04b1
Method        BLASTX
NCBI GI       g4455199
BLAST score    206
E value        4.0e-16
Match length   129
% identity     39
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      236027
Seq. ID       uC-gsflmaxxa098h05b1
Method        BLASTX
NCBI GI       g2984147
BLAST score    172
E value        2.0e-12
Match length   90
% identity     41
NCBI Description (AE000760) hypothetical protein [Aquifex aeolicus]
```

Seq. No.	236028
Seq. ID	uC-gsflmaxxa098h09b1
Method	BLASTX
NCBI GI	g3201618
BLAST score	588
E value	7.0e-61
Match length	128
% identity	84
NCBI Description	(AC004669) Sop2p-like protein [Arabidopsis thaliana]

34197

BLAST score	260
E value	1.0e-22
Match length	118
% identity	47
NCBI Description	(AC000106) F7G19.14 [Arabidopsis thaliana]
Seq. No.	236030
Seq. ID	uC-gsflmaxxa098h12b1
Method	BLASTX
NCBI GI	g2507229
BLAST score	518
E value	9.0e-53
Match length	133
% identity	74
NCBI Description	40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN) >gi_423247_pir_A46579 estrogen receptor-binding cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074) cyclophilin [Bos taurus]
Seq. No.	236031
Seq. ID	uC-gsflmaxxa106c02b1
Method	BLASTX
NCBI GI	g4325341
BLAST score	216
E value	9.0e-18
Match length	53
% identity	79
NCBI Description	(AF128393) similar to the Drosophila DES-1 protein (GB:X94180) [Arabidopsis thaliana]
Seq. No.	236032
Seq. ID	uC-gsflmaxxa107a01b1
Method	BLASTX
NCBI GI	g4049341
BLAST score	386
E value	2.0e-37
Match length	87
% identity	89
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	236033
Seq. ID	uC-gsflmaxxa107a07b1
Method	BLASTX
NCBI GI	g3335375
BLAST score	278
E value	3.0e-25
Match length	61
% identity	85
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]
Seq. No.	236034
Seq. ID	uC-gsflmaxxa107b12b1
Method	BLASTX
NCBI GI	g3694872
BLAST score	394

Match length	93
% identity	39
NCBI Description	(U89793) allergen Amb a VI [Ambrosia artemisiifolia]
Seq. No.	236040
Seq. ID	uC-gsflmaxxa119c02b1
Method	BLASTX
NCBI GI	g1076511
BLAST score	145
E value	1.0e-09
Match length	31
% identity	90
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]
Seq. No.	236041
Seq. ID	uC-gsflmaxxa119c07b1
Method	BLASTX
NCBI GI	g1916292
BLAST score	157
E value	1.0e-10
Match length	65
% identity	42
NCBI Description	(U89793) allergen Amb a VI [Ambrosia artemisiifolia]
Seq. No.	236042
Seq. ID	uC-gsflnu33B001a01b1
Method	BLASTX
NCBI GI	g2244898
BLAST score	364
E value	1.0e-34
Match length	150
% identity	46
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]
Seq. No.	236043
Seq. ID	uC-gsflnu33B001b03b1
Method	BLASTX
NCBI GI	g2739168
BLAST score	179
E value	6.0e-16
Match length	87
% identity	56
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]
Seq. No.	236044
Seq. ID	uC-gsflnu33B001b05b1
Method	BLASTX
NCBI GI	g1330401
BLAST score	133
E value	1.0e-08
Match length	76
% identity	46
NCBI Description	(U58762) T27F7.1 gene product [Caenorhabditis elegans]

Seq. No. 236045
 Seq. ID uC-gsflnu33B001b09b1
 Method BLASTX
 NCBI GI g3600052
 BLAST score 275
 E value 2.0e-24
 Match length 94
 % identity 56
 NCBI Description (AF080120) contains similarity to glycosyl hydrolases family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03) [Arabidopsis thaliana]

Seq. No. 236046
 Seq. ID uC-gsflnu33B001b11b1
 Method BLASTX
 NCBI GI g4322421
 BLAST score 233
 E value 2.0e-19
 Match length 133
 % identity 41
 NCBI Description (AF085230) cadmium resistance factor 1 [Arabidopsis thaliana]

Seq. No. 236047
 Seq. ID uC-gsflnu33B001c09b1
 Method BLASTX
 NCBI GI g1184075
 BLAST score 153
 E value 5.0e-10
 Match length 140
 % identity 3
 NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon esculentum]

Seq. No. 236048
 Seq. ID uC-gsflnu33B001d05b1
 Method BLASTX
 NCBI GI g2982268
 BLAST score 472
 E value 2.0e-47
 Match length 93
 % identity 98
 NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No. 236049
 Seq. ID uC-gsflnu33B001e09b1
 Method BLASTX
 NCBI GI g1816459
 BLAST score 531
 E value 3.0e-54
 Match length 133
 % identity 80
 NCBI Description (Y10750) DEFH125 protein [Antirrhinum majus]

BLAST score 417
 E value 6.0e-41
 Match length 89
 % identity 88
 NCBI Description (AC000106) Similar to Schizosaccharomyces CCAAT-binding factor (gb_U88525). EST gb_T04310 comes from this gene. [Arabidopsis thaliana]

Seq. No. 236071
 Seq. ID uC-gsflnu33B004h06b1
 Method BLASTX
 NCBI GI g2689720
 BLAST score 432
 E value 2.0e-57
 Match length 159
 % identity 73
 NCBI Description (AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No. 236072
 Seq. ID uC-gsflnu33B005b12b1
 Method BLASTX
 NCBI GI g2245061
 BLAST score 307
 E value 4.0e-28
 Match length 68
 % identity 87
 NCBI Description (Z97342) Clp proteinase homolog [Arabidopsis thaliana]

Seq. No. 236073
 Seq. ID uC-gsflnu33B005d02b1
 Method BLASTX
 NCBI GI g3757521
 BLAST score 470
 E value 3.0e-47
 Match length 132
 % identity 64
 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 236074
 Seq. ID uC-gsflnu33B005d03b1
 Method BLASTX
 NCBI GI g1703446
 BLAST score 497
 E value 2.0e-50
 Match length 130
 % identity 78
 NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
 >gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
 >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No. 236075
 Seq. ID uC-gsflnu33B005d08b1
 Method BLASTX
 NCBI GI g3894393
 BLAST score 185
 E value 7.0e-14

Seq. ID uC-gsflnu33B006c02b1
 Method BLASTX
 NCBI GI g2961343
 BLAST score 201
 E value 1.0e-15
 Match length 40
 % identity 95
 NCBI Description (AL022140) symbiosis-related like protein [Arabidopsis thaliana]

Seq. No. 236087
 Seq. ID uC-gsflnu33B006d02b1
 Method BLASTX
 NCBI GI g4490305
 BLAST score 407
 E value 9.0e-40
 Match length 147
 % identity 54
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 236088
 Seq. ID uC-gsflnu33B006f04b1
 Method BLASTX
 NCBI GI g120669
 BLAST score 252
 E value 8.0e-22
 Match length 59
 % identity 78
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
 dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
 >gi_19566_emb_CAA42905_(X60347) glyceraldehyde
 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 236089
 Seq. ID uC-gsflnu33B006f06b1
 Method BLASTX
 NCBI GI g1076257
 BLAST score 178
 E value 1.0e-13
 Match length 31
 % identity 97
 NCBI Description sucrose-proton symporter - beet >gi_633172_emb_CAA58730_
 (X83850) sucrose/proton-symporter [Beta vulgaris]

Seq. No. 236090
 Seq. ID uC-gsflnu33B006g07b1
 Method BLASTX
 NCBI GI g2961390
 BLAST score 347
 E value 7.0e-33
 Match length 84
 % identity 74
 NCBI Description (AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No. 236091

Seq. ID uC-gsflnu33B006g12b1
 Method BLASTX
 NCBI GI g4115937
 BLAST score 301
 E value 7.0e-39
 Match length 101
 % identity 75
 NCBI Description (AF118223) contains similarity to human PCF11p homolog
 (GB:AF046935) [Arabidopsis thaliana]

Seq. No. 236092
 Seq. ID uC-gsflnu33B006h10b1
 Method BLASTX
 NCBI GI g2983537
 BLAST score 147
 E value 2.0e-09
 Match length 55
 % identity 53
 NCBI Description (AE000720) phosphate transport ATP binding protein [Aquifex
 aeolicus]

Seq. No. 236093
 Seq. ID uC-gsflnu33B006h11b1
 Method BLASTX
 NCBI GI g2583112
 BLAST score 153
 E value 1.0e-10
 Match length 42
 % identity 67
 NCBI Description (AC002387) putative PD1-like DNA-binding protein
 [Arabidopsis thaliana]

Seq. No. 236094
 Seq. ID uC-gsflnu33B008a04b1
 Method BLASTX
 NCBI GI g4539401
 BLAST score 289
 E value 7.0e-26
 Match length 109
 % identity 61
 NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

Seq. No. 236095
 Seq. ID uC-gsflnu33B008b01b1
 Method BLASTX
 NCBI GI g1706794
 BLAST score 361
 E value 3.0e-34
 Match length 121
 % identity 55
 NCBI Description BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE
 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE)
 (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE)
 (FRAGILE HISTIDINE TRIAD PROTEIN) >gi_3114520_pdb_4FIT_
 Fhit-Apo >gi_3114524_pdb_6FIT_ Fhit-Transition State
 Analog >gi_3318895_pdb_1FHI_ Substrate Analog (Ib2)
 Complex With The Fragile Histidine Triad Protein, Fhit

0963-016-101000

```
Seq. No.      236097
Seq. ID       uC-gsflnu33B008b12b1
Method        BLASTX
NCBI GI       g1914685
BLAST score    283
E value        2.0e-25
Match length   113
% identity     54
NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]
```

```
Seq. No.      236099
Seq. ID       uC-gsflnu33B008c10b1
Method        BLASTX
NCBI GI       g4539373
BLAST score   142
E value       7.0e-09
Match length  84
% identity    38
NCBI Description (AL049525) putative retrotransposon polyprotein
                [Arabidopsis thaliana]
```

34211


```
% identity      90
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
```

Seq. No.	236101
Seq. ID	uC-gsflnu33B008e09b1
Method	BLASTX
NCBI GI	g2982309
BLAST score	167
E value	1.0e-23
Match length	98

```
% identity      50
NCBI Description (AF051239) probable ubiquitin activating enzyme 2 [Picea
mariana]
```

```
Seq. No.          236102
Seq. ID           uC-gsflnu33B008f06b1
Method            BLASTX
NCBI GI           g3420239
BLAST score       261
E value           3.0e-23
Match length      49
% identity        100
NCBI Description  (AF059484) actin [Gossypium hirsutum]
```

```
Seq. No.      236103
Seq. ID      uC-gsflnu33B008f12b1
Method       BLASTX
NCBI GI      g1174448
BLAST score   162
E value      4.0e-11
Match length  75
% identity    49
NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
                (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative
                [Arabidopsis thaliana]
```

```
Seq. No..      236104
Seq. ID       uC-gsflnu33B008g12b1
Method        BLASTX
NCBI GI       g4185143
BLAST score    246
E value       3.0e-21
Match length   72
% identity     64
NCBI Description (AC005724) putative signal recognition particle receptor
beta subunit [Arabidopsis thaliana]
```

```
Seq. No.      236105
Seq. ID      uC-gsflnu33B008h05b1
Method       BLASTX
NCBI GI      g967125
BLAST score   444
E value      2.0e-44
Match length  91
% identity    95
NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]
```


Method BLASTX
 NCBI GI g3335359
 BLAST score 488
 E value 3.0e-49
 Match length 106
 % identity 87
 NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 236112
 Seq. ID uC-gsflnu33B009h11b1
 Method BLASTX
 NCBI GI g4432840
 BLAST score 173
 E value 2.0e-12
 Match length 95
 % identity 42
 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 236113
 Seq. ID uC-gsflnu33B011a02b1
 Method BLASTX
 NCBI GI g3080417
 BLAST score 346
 E value 9.0e-33
 Match length 89
 % identity 83
 NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 236114
 Seq. ID uC-gsflnu33B011b05b1
 Method BLASTX
 NCBI GI g2529670
 BLAST score 236
 E value 8.0e-20
 Match length 79
 % identity 61
 NCBI Description (AC002535) ribosomal protein L18-like [Arabidopsis thaliana]

Seq. No. 236115
 Seq. ID uC-gsflnu33B011d04b1
 Method BLASTX
 NCBI GI g3220021
 BLAST score 224
 E value 3.0e-23
 Match length 125
 % identity 46
 NCBI Description (U57828) lipase homolog [Arabidopsis thaliana]

Seq. No. 236116
 Seq. ID uC-gsflnu33B011d07b1
 Method BLASTX
 NCBI GI g4105633
 BLAST score 204
 E value 6.0e-16
 Match length 56
 % identity 71

Method BLASTX
 NCBI GI g1717744
 BLAST score 222
 E value 5.0e-18
 Match length 108
 % identity 42
 NCBI Description TOPOISOMERASE 1-RELATED PROTEIN TRF4
 >gi_1077298_pir_S51882 topoisomerase I-related protein
 TRF4 - yeast (*Saccharomyces cerevisiae*)
 >gi_663237_emb_CAA88145_(Z48149) ORF [*Saccharomyces*
cerevisiae] >gi_950226 (U31355) Trf4p [*Saccharomyces*
cerevisiae] >gi_1419987_emb_CAA99134_(Z74857) ORF YOL115w
 [*Saccharomyces cerevisiae*]

Seq. No. 236123
 Seq. ID uC-gsflnu33B011g09b1
 Method BLASTX
 NCBI GI g2213600
 BLAST score 161
 E value 2.0e-11
 Match length 80
 % identity 46
 NCBI Description (AC000348) T7N9.20 [*Arabidopsis thaliana*]

Seq. No. 236124
 Seq. ID uC-gsflnu33B011h06b1
 Method BLASTX
 NCBI GI g3953470
 BLAST score 149
 E value 1.0e-09
 Match length 80
 % identity 49
 NCBI Description (AC002328) F20N2.15 [*Arabidopsis thaliana*]

Seq. No. 236125
 Seq. ID uC-gsflnu33B012c08b1
 Method BLASTX
 NCBI GI g3832528
 BLAST score 524
 E value 1.0e-53
 Match length 126
 % identity 81
 NCBI Description (AF100167) unknown [*Glycine max*]

Seq. No. 236126
 Seq. ID uC-gsflnu33B012d01b1
 Method BLASTX
 NCBI GI g3287693
 BLAST score 434
 E value 5.0e-43
 Match length 90
 % identity 89
 NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from
 the genome of *Synechocystis* sp. gb_D90916. [*Arabidopsis*
thaliana]

Seq. No. 236127

Seq. ID uC-gsflnu33B012e08b1
 Method BLASTX
 NCBI GI g2062170
 BLAST score 272
 E value 5.0e-24
 Match length 136
 % identity 52
 NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]

Seq. No. 236128
 Seq. ID uC-gsflnu33B012g08b1
 Method BLASTX
 NCBI GI g2244847
 BLAST score 246
 E value 5.0e-21
 Match length 105
 % identity 54
 NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No. 236129
 Seq. ID uC-gsflnu33B013a03b1
 Method BLASTX
 NCBI GI g3647283
 BLAST score 554
 E value 5.0e-57
 Match length 144
 % identity 74
 NCBI Description (AJ011418) ubiquitin activating enzyme [Lycopersicon esculentum]

Seq. No. 236130
 Seq. ID uC-gsflnu33B013a06b1
 Method BLASTX
 NCBI GI g1587206
 BLAST score 363
 E value 8.0e-56
 Match length 148
 % identity 80
 NCBI Description T complex protein [Cucumis sativus]

Seq. No. 236131
 Seq. ID uC-gsflnu33B013a07b1
 Method BLASTX
 NCBI GI g4115377
 BLAST score 196
 E value 4.0e-15
 Match length 94
 % identity 43
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 236132
 Seq. ID uC-gsflnu33B013a10b1
 Method BLASTX
 NCBI GI g2213626
 BLAST score 239
 E value 5.0e-20

Match length 120
 % identity 42
 NCBI Description (AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No. 236133
 Seq. ID uC-gsflnu33B013b10b1
 Method BLASTX
 NCBI GI g2244759
 BLAST score 542
 E value 1.0e-55
 Match length 137
 % identity 72
 NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 236134
 Seq. ID uC-gsflnu33B013b11b1
 Method BLASTX
 NCBI GI g3928084
 BLAST score 515
 E value 2.0e-52
 Match length 152
 % identity 64
 NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No. 236135
 Seq. ID uC-gsflnu33B013f11b1
 Method BLASTX
 NCBI GI g1352186
 BLAST score 523
 E value 3.0e-53
 Match length 123
 % identity 77
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 236136
 Seq. ID uC-gsflnu33B013f12b1
 Method BLASTX
 NCBI GI g4567262
 BLAST score 520
 E value 6.0e-63
 Match length 132
 % identity 89
 NCBI Description (AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No. 236137
 Seq. ID uC-gsflnu33B015a03b1
 Method BLASTX
 NCBI GI g4455340
 BLAST score 466
 E value 1.0e-46
 Match length 131
 % identity 66
 NCBI Description (AL035522) putative protein [Arabidopsis thaliana]

Seq. No. 236138
 Seq. ID uC-gsflnu33B015a04b1
 Method BLASTX
 NCBI GI g1723894
 BLAST score 272
 E value 7.0e-24
 Match length 164
 % identity 40
 NCBI Description HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC
 REGION >gi_2131584_pir_S64106 hypothetical protein YGL099w
 - yeast (*Saccharomyces cerevisiae*)
 >gi_1322637_emb_CAA96805_ (Z72621) ORF YGL099w
 [*Saccharomyces cerevisiae*]

Seq. No. 236139
 Seq. ID uC-gsflnu33B015a09b1
 Method BLASTX
 NCBI GI g464707
 BLAST score 571
 E value 4.0e-59
 Match length 117
 % identity 95
 NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal
 protein S18.A - *Arabidopsis thaliana*
 >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
 [*Arabidopsis thaliana*] >gi_434343_emb_CAA82273_ (Z28701)
 S18 ribosomal protein [*Arabidopsis thaliana*]
 >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
 [*Arabidopsis thaliana*] >gi_434906_emb_CAA82275_ (Z28962)
 S18 ribosomal protein [*Arabidopsis thaliana*]
 >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
 [*Arabidopsis thaliana*] >gi_3287678 (AC003979) Match to
 ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
 thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
 gb_R30430 come from this gene. [*Arabidopsis thaliana*]
 >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
 protein [*Arabidopsis thaliana*]

Seq. No. 236140
 Seq. ID uC-gsflnu33B015b01b1
 Method BLASTX
 NCBI GI g3334157
 BLAST score 516
 E value 4.0e-70
 Match length 155
 % identity 82
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
 (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
 >gi_1220142_emb_CAA59468_ (X85185) cyclophilin
 [*Catharanthus roseus*]

Seq. No. 236141
 Seq. ID uC-gsflnu33B015b09b1
 Method BLASTX
 NCBI GI g4376203
 BLAST score 343
 E value 3.0e-32

NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana]
>gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]

Seq. No. 236147
Seq. ID uC-gsflnu33B015g08b1
Method BLASTX
NCBI GI g4309730
BLAST score 232
E value 4.0e-19
Match length 111
% identity 44

NCBI Description (AC006439) putative lipid transfer protein [Arabidopsis thaliana]

Seq. No. 236148
Seq. ID uC-gsflnu33B015h09b1
Method BLASTX
NCBI GI g4467096
BLAST score 526
E value 1.0e-53
Match length 152
% identity 47

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 236149
Seq. ID uC-gsflnu33B016a06b1
Method BLASTX
NCBI GI g3719211
BLAST score 209
E value 1.0e-16
Match length 44
% identity 89
NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

Seq. No. 236150
Seq. ID uC-gsflnu33B016a08b1
Method BLASTX
NCBI GI g4468804
BLAST score 317
E value 3.0e-29
Match length 146
% identity 19
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 236151
Seq. ID uC-gsflnu33B016b10b1
Method BLASTX
NCBI GI g231757
BLAST score 768
E value 5.0e-82
Match length 167
% identity 88
NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
(S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
3-O-METHYLTRANSFERASE) (COMT) >gi_99653_pir_S18568
lignin-bispecific O-methyltransferase (EC 2.1.1.-) -

0968416 : 101000

BLAST score 314
 E value 6.0e-29
 Match length 76
 % identity 83
 NCBI Description (AF076275) contains similarity to Caenorhabditis elegans MEL-26 (GB:U67737) [Arabidopsis thaliana]

Seq. No. 236157
 Seq. ID uC-gsflnu33B016f12b1
 Method BLASTX
 NCBI GI g2809246
 BLAST score 347
 E value 8.0e-33
 Match length 123
 % identity 59
 NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 236158
 Seq. ID uC-gsflnu33B016g05b1
 Method BLASTX
 NCBI GI g1480012
 BLAST score 157
 E value 7.0e-11
 Match length 30
 % identity 93
 NCBI Description (D78492) putative ubiquitin extension protein [Brassica rapa]

Seq. No. 236159
 Seq. ID uC-gsflnu33B016g06b1
 Method BLASTX
 NCBI GI g585628
 BLAST score 164
 E value 2.0e-11
 Match length 40
 % identity 78
 NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1 CATALYTIC SUBUNIT >gi_418779_pir_S31162 phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain (clone EP14a) - Arabidopsis thaliana >gi_166823 (M96733) protein phosphatase [Arabidopsis thaliana]

Seq. No. 236160
 Seq. ID uC-gsflnu33B016g09b1
 Method BLASTX
 NCBI GI g132935
 BLAST score 214
 E value 2.0e-17
 Match length 65
 % identity 60
 NCBI Description 60S RIBOSOMAL PROTEIN L37A (YL37) (RP47)
 >gi_101568_pir_S18431 ribosomal protein L35a.e.c16 - yeast (Saccharomyces cerevisiae) >gi_4392_emb_CAA41035_ (X57969) ribosomal protein L37a [Saccharomyces cerevisiae]
 >gi_1244773 (U43703) Lpi4p [Saccharomyces cerevisiae]
 >gi_1370305_emb_CAA97847_ (Z73499) ORF YPL143w [Saccharomyces cerevisiae]

cv. Alexis, aleurone, Peptide, 516 aa]
 >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
 [Hordeum vulgare]

Seq. No. 236177
 Seq. ID uC-gsflnu33B018h08b1
 Method BLASTX
 NCBI GI g4417304
 BLAST score 379
 E value 1.0e-36
 Match length 100
 % identity 63
 NCBI Description (AC006446) putative beta-1,4-mannosyl-glycoprotein
 beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
 thaliana]

Seq. No. 236178
 Seq. ID uC-gsflnu33B019a02b1
 Method BLASTX
 NCBI GI g3776084
 BLAST score 223
 E value 4.0e-18
 Match length 83
 % identity 48
 NCBI Description (Y18251) NtN2 [Medicago truncatula]

Seq. No. 236179
 Seq. ID uC-gsflnu33B019b01b1
 Method BLASTX
 NCBI GI g4558673
 BLAST score 311
 E value 1.0e-28
 Match length 134
 % identity 37
 NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236180
 Seq. ID uC-gsflnu33B019b10b1
 Method BLASTX
 NCBI GI g3004565
 BLAST score 259
 E value 1.0e-22
 Match length 94
 % identity 23
 NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 236181
 Seq. ID uC-gsflnu33B019c05b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 9.0e-15
 Match length 47
 % identity 68
 NCBI Description (AF116845) metallothionein-like type 1 protein. [Ipomoea
 batatas]

NCBI GI g3367523
 BLAST score 185
 E value 1.0e-23
 Match length 74
 % identity 69
 NCBI Description (AC004392) ESTs gb_AA728658 and gb_N95943 come from this gene. [Arabidopsis thaliana]

Seq. No. 236188
 Seq. ID uC-gsflnu33B019h06b1
 Method BLASTX
 NCBI GI g2980641
 BLAST score 194
 E value 3.0e-20
 Match length 89
 % identity 44
 NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No. 236189
 Seq. ID uC-gsflnu33B019h09b1
 Method BLASTX
 NCBI GI g2213610
 BLAST score 377
 E value 3.0e-36
 Match length 105
 % identity 27
 NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No. 236190
 Seq. ID uC-gsflnu33B019h12b1
 Method BLASTX
 NCBI GI g2623309
 BLAST score 313
 E value 8.0e-29
 Match length 130
 % identity 52
 NCBI Description (AC002409) similar to tgacg-specific DNA-binding protein [Arabidopsis thaliana]

Seq. No. 236191
 Seq. ID uC-gsflnu33B022a12b1
 Method BLASTX
 NCBI GI g4204259
 BLAST score 333
 E value 4.0e-31
 Match length 108
 % identity 68
 NCBI Description (AC005223) 18074 [Arabidopsis thaliana]

Seq. No. 236192
 Seq. ID uC-gsflnu33B022b03b1
 Method BLASTX
 NCBI GI g4539660
 BLAST score 388
 E value 1.0e-37
 Match length 107
 % identity 66

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 236193
Seq. ID uC-gsflnu33B022b06b1
Method BLASTX
NCBI GI g3880625
BLAST score 248
E value 4.0e-21
Match length 82
% identity 54
NCBI Description (Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge

Seq. No. 236194
Seq. ID uC-gsflnu33B022f07b1
Method BLASTX
NCBI GI g2262099
BLAST score 466
E value 7.0e-47
Match length 99
% identity 79
NCBI Description (AC002343) thaumatin isolog [Arabidopsis thaliana]

Seq. No. 236195
Seq. ID uC-gsflnu33B022g04b1
Method BLASTX
NCBI GI g2507442
BLAST score 147
E value 2.0e-09
Match length 29
% identity 93
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1419685_emb_CAA67207_ (X98618) TCTP-like protein [Medicago sativa]

Seq. No. 236196
Seq. ID uC-gsflnu33B023a10b1
Method BLASTX
NCBI GI g913227
BLAST score 209
E value 3.0e-17
Match length 59
% identity 68
NCBI Description transcription factor X1DP-1 [Xenopus laevis, embryos, Peptide, 409 aa]

Seq. No. 236197
Seq. ID uC-gsflnu33B023a11b1
Method BLASTX
NCBI GI g3892047
BLAST score 158
E value 1.0e-10
Match length 107
% identity 37

NCBI Description (AC002330) putative bZIP-like DNA binding protein
[Arabidopsis thaliana]

Seq. No. 236198
Seq. ID uC-gsflnu33B023d05b1
Method BLASTX
NCBI GI g1296816
BLAST score 377
E value 3.0e-36
Match length 88
% identity 84
NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.]

Seq. No. 236199
Seq. ID uC-gsflnu33B023f01b1
Method BLASTX
NCBI GI g1076620
BLAST score 334
E value 2.0e-31
Match length 92
% identity 67
NCBI Description cyclin - common tobacco >gi_599933_emb_CAA86032_ (Z37978)
Cyclin [Nicotiana tabacum]

Seq. No. 236200
Seq. ID uC-gsflnu33B023f04b1
Method BLASTX
NCBI GI g2462925
BLAST score 138
E value 1.0e-08
Match length 33
% identity 82
NCBI Description (AJ000053) GTP cyclohydrolase II /
3,4-dihydroxy-2-butanone-4-phosphate synthase [Arabidopsis
thaliana]

Seq. No. 236201
Seq. ID uC-gsflnu33B023f12b1
Method BLASTX
NCBI GI g1532167
BLAST score 147
E value 2.0e-09
Match length 48
% identity 52
NCBI Description (U63815) localized according to blastn similarity to EST
sequences; therefore, the coding span corresponds only to
an area of similarity since the initiation codon and stop
codon could not be precisely determined [Arabidopsis
thaliana]

Seq. No. 236202
Seq. ID uC-gsflnu33B023g01b1
Method BLASTX
NCBI GI g4154352
BLAST score 174
E value 1.0e-12
Match length 91

% identity	42
NCBI Description	(AF110333) PrMC3 [Pinus radiata]
Seq. No.	236203
Seq. ID	uC-gsflnu33B023h04b1
Method	BLASTX
NCBI GI	g2618689
BLAST score	672
E value	7.0e-71
Match length	149
% identity	88
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.	236204
Seq. ID	uC-gsflnu33B023h11b1
Method	BLASTX
NCBI GI	g4309759
BLAST score	327
E value	8.0e-31
Match length	86
% identity	78
NCBI Description	(AC006217) unknown protein with Src homology 3 (SH3) domain profile (PDOC50002) [Arabidopsis thaliana]
Seq. No.	236205
Seq. ID	uC-gsflnu33B024d09b1
Method	BLASTX
NCBI GI	g3776573
BLAST score	259
E value	5.0e-23
Match length	63
% identity	71
NCBI Description	(AC005388) Similar to nodulins and lipase homolog F14J9.5 gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis thaliana]
Seq. No.	236206
Seq. ID	uC-gsflnu33B024g09b1
Method	BLASTX
NCBI GI	g2832632
BLAST score	146
E value	2.0e-09
Match length	52
% identity	54
NCBI Description	(AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.	236207
Seq. ID	uC-gsflnu33B025b07b1
Method	BLASTX
NCBI GI	g4415924
BLAST score	218
E value	3.0e-18
Match length	53
% identity	68
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No. 236208
 Seq. ID uC-gsflnu33B025b11b1
 Method BLASTX
 NCBI GI g3169719
 BLAST score 355
 E value 3.0e-34
 Match length 77
 % identity 88
 NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]

Seq. No. 236209
 Seq. ID uC-gsflnu33B025g07b1
 Method BLASTX
 NCBI GI g401189
 BLAST score 281
 E value 1.0e-25
 Match length 59
 % identity 88
 NCBI Description WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP) (TURGOR-RESPONSIVE PROTEIN 7A) >gi_485511_pir_S33617 trg-31 protein - garden pea >gi_20426_emb_CAA79159_ (Z18288) trg-31 [Pisum sativum]

Seq. No. 236210
 Seq. ID uC-gsflnu33B025g11b1
 Method BLASTX
 NCBI GI g633110
 BLAST score 157
 E value 5.0e-11
 Match length 34
 % identity 100
 NCBI Description (D31843) plasma membrane H⁺-ATPase [Oryza sativa]

Seq. No. 236211
 Seq. ID uC-gsflnu33B026a02b1
 Method BLASTX
 NCBI GI g4406819
 BLAST score 193
 E value 1.0e-14
 Match length 81
 % identity 51
 NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]

Seq. No. 236212
 Seq. ID uC-gsflnu33B026b10b1
 Method BLASTX
 NCBI GI g3005576
 BLAST score 642
 E value 2.0e-67
 Match length 134
 % identity 53
 NCBI Description (AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]

Seq. No. 236213
 Seq. ID uC-gsflnu33B026d04b1

BLAST score 502
 E value 6.0e-51
 Match length 130
 % identity 75
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 236219
 Seq. ID uC-gsflnu33B026h10b1
 Method BLASTX
 NCBI GI g4101564
 BLAST score 244
 E value 1.0e-20
 Match length 122
 % identity 46
 NCBI Description (AF004556) IFA-binding protein [Arabidopsis thaliana]

Seq. No. 236220
 Seq. ID uC-gsflnu33B027a01b1
 Method BLASTX
 NCBI GI g2245096
 BLAST score 216
 E value 1.0e-17
 Match length 78
 % identity 62
 NCBI Description (Z97343) inositol 2-dehydrogenase homolog [Arabidopsis thaliana]

Seq. No. 236221
 Seq. ID uC-gsflnu33B027a02b1
 Method BLASTX
 NCBI GI g4539301
 BLAST score 219
 E value 8.0e-18
 Match length 114
 % identity 38
 NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 236222
 Seq. ID uC-gsflnu33B027a09b1
 Method BLASTX
 NCBI GI g3367534
 BLAST score 526
 E value 9.0e-54
 Match length 139
 % identity 76
 NCBI Description (AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 236223
 Seq. ID uC-gsflnu33B027b12b1
 Method BLASTX
 NCBI GI g1621467
 BLAST score 633
 E value 3.0e-66
 Match length 161

E value 2.0e-50
 Match length 102
 % identity 93
 NCBI Description H+-transporting ATPase (EC 3.6.1.35) (clone PHA1) - potato
 >gi_435003_emb_CAA54046_ (X76536) H(+)-transporting ATPase
 [Solanum tuberosum]

Seq. No. 236229
 Seq. ID uC-gsflnu33B027g02b1
 Method BLASTX
 NCBI GI g1171978
 BLAST score 278
 E value 3.0e-25
 Match length 80
 % identity 18
 NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
 (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
 [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
 poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 236230
 Seq. ID uC-gsflnu33B027h04b1
 Method BLASTX
 NCBI GI g3850818
 BLAST score 390
 E value 7.0e-38
 Match length 90
 % identity 77
 NCBI Description (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
 sativa]

Seq. No. 236231
 Seq. ID uC-gsflnu33B028a04b1
 Method BLASTX
 NCBI GI g2781362
 BLAST score 200
 E value 7.0e-16
 Match length 89
 % identity 23
 NCBI Description (AC003113) F2401.18 [Arabidopsis thaliana]

Seq. No. 236232
 Seq. ID uC-gsflnu33B028b04b1
 Method BLASTX
 NCBI GI g3142292
 BLAST score 543
 E value 1.0e-55
 Match length 125
 % identity 79
 NCBI Description (AC002411) Contains similarity to tetratricopeptide repeat
 protein gb_U46571 from homo sapiens. EST gb_Z47802 and
 gb_Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No. 236233
 Seq. ID uC-gsflnu33B028b08b1
 Method BLASTX
 NCBI GI g1076510

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thaliana]

Seq. No. 236249
 Seq. ID uC-gsflnu33B035a08b1
 Method BLASTX
 NCBI GI g2829918
 BLAST score 312
 E value 1.0e-28
 Match length 123
 % identity 54
 NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No. 236250
 Seq. ID uC-gsflnu33B035a12b1
 Method BLASTX
 NCBI GI g2281449
 BLAST score 224
 E value 2.0e-18
 Match length 86
 % identity 55
 NCBI Description (U90214) leucine zipper transcription factor TGA2.1 [Nicotiana tabacum]

Seq. No. 236251
 Seq. ID uC-gsflnu33B035b05b1
 Method BLASTX
 NCBI GI g2583108
 BLAST score 243
 E value 4.0e-21
 Match length 70
 % identity 70
 NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No. 236252
 Seq. ID uC-gsflnu33B035c07b1
 Method BLASTX
 NCBI GI g3738316
 BLAST score 363
 E value 1.0e-34
 Match length 106
 % identity 67
 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 236253
 Seq. ID uC-gsflnu33B035d07b1
 Method BLASTX
 NCBI GI g2270994
 BLAST score 134
 E value 3.0e-10
 Match length 99
 % identity 42
 NCBI Description (AF004809) Ca²⁺-binding EF hand protein [Glycine max]

Seq. No. 236254
 Seq. ID uC-gsflnu33B035d12b1
 Method BLASTX

Match length 58
 % identity 62
 NCBI Description (AF013293) contains weak similarity to *S. cerevisiae* BOB1 protein (PIR:S45444) [*Arabidopsis thaliana*]

Seq. No. 236265
 Seq. ID uC-gsflnu33B037d06b1
 Method BLASTX
 NCBI GI g2342725
 BLAST score 309
 E value 3.0e-28
 Match length 141
 % identity 48
 NCBI Description (AC002341) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 236266
 Seq. ID uC-gsflnu33B037e11b1
 Method BLASTX
 NCBI GI g4262228
 BLAST score 368
 E value 2.0e-35
 Match length 111
 % identity 74
 NCBI Description (AC006200) putative receptor protein kinase [*Arabidopsis thaliana*]

Seq. No. 236267
 Seq. ID uC-gsflnu33B037f01b1
 Method BLASTX
 NCBI GI g3024516
 BLAST score 317
 E value 8.0e-45
 Match length 118
 % identity 86
 NCBI Description RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong similarity to *A. thaliana* ara-2 (gb_ATHARA2). ESTs gb_ATTS2483, gb_ATTS2484, gb_AA042159 come from this gene. [*Arabidopsis thaliana*] >gi_2231303 (U74669) ras-related small GTPase [*Arabidopsis thaliana*]

Seq. No. 236268
 Seq. ID uC-gsflnu33B037h09b1
 Method BLASTX
 NCBI GI g2281090
 BLAST score 307
 E value 1.0e-28
 Match length 75
 % identity 84
 NCBI Description (AC002333) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 236269
 Seq. ID uC-gsflnu33B046a09b1
 Method BLASTX
 NCBI GI g4455323
 BLAST score 143
 E value 4.0e-09
 Match length 63


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Seq. No.          236280
Seq. ID           uC-gsflnu33B049d04b1
Method            BLASTX
NCBI GI           g464981
BLAST score       393
E value           4.0e-38
Match length      74
% identity        99
NCBI Description   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
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Seq. No.      236281
Seq. ID       uC-gsflnu33B049e06b1
Method        BLASTX
NCBI GI       g416641
BLAST score   229
E value       2.0e-19
Match length  48
% identity    85
NCBI Description  INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4
                >gi_287568_dbj_BAA03309_(D14413) ORF [Vigna radiata]
```

```
Seq. No.          236282
Seq. ID           uC-gsflnu33B049e08b1
Method            BLASTX
NCBI GI           g4100433
BLAST score       240
E value           2.0e-20
Match length      72
% identity        56
NCBI Description   (AF000378) beta-glucosidase [Glycine max]
```

```
Seq. No.      236283
Seq. ID       uC-gsflnu33B049f01b1
Method        BLASTX
NCBI GI       g1707015
BLAST score    345
E value        9.0e-33
Match length   101
% identity     65
NCBI Description (U78721) protein phosphatase 2C isolog [Arabidopsis
                thaliana]
```

```
Seq. No.          236284
Seq. ID           uC-gsflnu33B049f09b1
Method            BLASTX
NCBI GI           g3789940
BLAST score       216
E value           5.0e-18
Match length      47
% identity        23
NCBI Description  (AF093504) tetra-ubiquitin [Saccharum hybrid cultivar
                  H32-8560]
```

Seq. No. 236285

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Match length	137
% identity	44
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	236296
Seq. ID	uC-gsflnu33B051a02b1
Method	BLASTX
NCBI GI	g2104536
BLAST score	458
E value	9.0e-46
Match length	99
% identity	77
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]
Seq. No.	236297
Seq. ID	uC-gsflnu33B051a08b1
Method	BLASTX
NCBI GI	g3913724
BLAST score	329
E value	5.0e-31
Match length	74
% identity	88
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-2 SUBUNIT (GP-ALPHA-2) >gi_1834453_emb_CAA64834_ (X95582) G protein [Glycine max]
Seq. No.	236298
Seq. ID	uC-gsflnu33B051b04b1
Method	BLASTX
NCBI GI	g553111
BLAST score	143
E value	1.0e-08
Match length	91
% identity	11
NCBI Description	(J03625) hydroproline-rich protein [Glycine max]
Seq. No.	236299
Seq. ID	uC-gsflnu33B051c02b1
Method	BLASTX
NCBI GI	g3935171
BLAST score	252
E value	1.0e-21
Match length	55
% identity	84
NCBI Description	(AC004557) F17L21.14 [Arabidopsis thaliana]
Seq. No.	236300
Seq. ID	uC-gsflnu33B051e02b1
Method	BLASTX
NCBI GI	g3413697
BLAST score	200
E value	2.0e-15
Match length	150
% identity	39
NCBI Description	(AC004747) SF16-like protein, 5' partial [Arabidopsis thaliana]

Seq. No. 236301
 Seq. ID uC-gsflnu33B051f03b1
 Method BLASTX
 NCBI GI g3914430
 BLAST score 205
 E value 2.0e-16
 Match length 64
 % identity 61
 NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]

Seq. No. 236302
 Seq. ID uC-gsflnu33B051g02b1
 Method BLASTX
 NCBI GI g548441
 BLAST score 250
 E value 5.0e-22
 Match length 45
 % identity 98
 NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT >gi_486805_pir_S35502 phosphoprotein phosphatase (EC 3.1.3.16) 2A - alfalfa >gi_287811_emb_CAA49849_ (X70399) phosphoprotein phosphatase type 2A [Medicago sativa]

Seq. No. 236303
 Seq. ID uC-gsflnu33B051g07b1
 Method BLASTX
 NCBI GI g538067
 BLAST score 164
 E value 1.0e-11
 Match length 90
 % identity 44
 NCBI Description (M77661) putative pol polyprotein [Magnaporthe grisea]

Seq. No. 236304
 Seq. ID uC-gsflnu33B051h12b1
 Method BLASTX
 NCBI GI g1076402
 BLAST score 159
 E value 9.0e-11
 Match length 112
 % identity 38
 NCBI Description S-like ribonuclease RNS2 - Arabidopsis thaliana

Seq. No. 236305
 Seq. ID uC-gsflnu33B055a06b1
 Method BLASTX
 NCBI GI g2104536
 BLAST score 263
 E value 4.0e-23
 Match length 65
 % identity 69
 NCBI Description (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No. 236306
 Seq. ID uC-gsflnu33B055a12b1
 Method BLASTX
 NCBI GI g2623304
 BLAST score 229
 E value 6.0e-19
 Match length 131
 % identity 39
 NCBI Description (AC002409) similar to Medicago nodulin N21 [Arabidopsis thaliana]

Seq. No. 236307
 Seq. ID uC-gsflnu33B055c02b1
 Method BLASTX
 NCBI GI g4206209
 BLAST score 531
 E value 3.0e-54
 Match length 155
 % identity 67
 NCBI Description (AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No. 236308
 Seq. ID uC-gsflnu33B055c10b1
 Method BLASTX
 NCBI GI g3402672
 BLAST score 396
 E value 1.0e-38
 Match length 106
 % identity 71
 NCBI Description (AC004697) putative white protein [Arabidopsis thaliana]

Seq. No. 236309
 Seq. ID uC-gsflnu33B055e08b1
 Method BLASTX
 NCBI GI g1542941
 BLAST score 244
 E value 1.0e-20
 Match length 59
 % identity 86
 NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No. 236310
 Seq. ID uC-gsflnu33B055g04b1
 Method BLASTX
 NCBI GI g113217
 BLAST score 183
 E value 6.0e-14
 Match length 37
 % identity 95
 NCBI Description ACTIN 1 >gi_100149_pir__S07002 actin 1 - carrot

Seq. No. 236311
 Seq. ID uC-gsflnu33B055g06b1
 Method BLASTX

% identity 49
 NCBI Description (AC003974) putative cytochrome b5 [Arabidopsis thaliana]

 Seq. No. 236326
 Seq. ID uC-gsflnu33B057h05b1
 Method BLASTX
 NCBI GI g3881189
 BLAST score 210
 E value 1.0e-16
 Match length 71
 % identity 54
 NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No. 236327
 Seq. ID uC-gsflnu33B057h11b1
 Method BLASTX
 NCBI GI g2190542
 BLAST score 416
 E value 7.0e-41
 Match length 139
 % identity 61
 NCBI Description (AC001229) F5I14.5 gene product [Arabidopsis thaliana]

Seq. No. 236328
 Seq. ID uC-gsflnu33B058a04b1
 Method BLASTX
 NCBI GI g2462741
 BLAST score 179
 E value 1.0e-13
 Match length 38
 % identity 87
 NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 236329
 Seq. ID uC-gsflnu33B058a09b1
 Method BLASTX
 NCBI GI g3800878
 BLAST score 357
 E value 3.0e-34
 Match length 90
 % identity 80
 NCBI Description (AF096281) threonine dehydratase/deaminase [Arabidopsis thaliana]

Seq. No. 236330
 Seq. ID uC-gsflnu33B058d01b1
 Method BLASTX
 NCBI GI g3892059
 BLAST score 190
 E value 3.0e-14
 Match length 67
 % identity 63
 NCBI Description (AC002330) predicted protein of unknown function

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

34257

NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No. 236341
Seq. ID uC-gsflnu33B059c01b1
Method BLASTX
NCBI GI g2842493
BLAST score 346
E value 1.0e-32
Match length 105
% identity 64

NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 236342
Seq. ID uC-gsflnu33B059d10b1
Method BLASTX
NCBI GI g3242077
BLAST score 504
E value 4.0e-51
Match length 140
% identity 69

NCBI Description (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 236343
Seq. ID uC-gsflnu33B059e11b1
Method BLASTX
NCBI GI g2558962
BLAST score 422
E value 2.0e-41
Match length 86
% identity 100

NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No. 236344
Seq. ID uC-gsflnu33B059f03b1
Method BLASTX
NCBI GI g3249070
BLAST score 475
E value 1.0e-47
Match length 144
% identity 73

NCBI Description (AC004473) Contains similarity to siah binding protein 1 (SiahBP1) gb_U51586 from Homo sapiens. ESTs gb_T43314, gb_T43315 and gb_R90521, gb_T75905 [Arabidopsis thaliana]

Seq. No. 236345
Seq. ID uC-gsflnu33B059f07b1
Method BLASTX
NCBI GI g1076746
BLAST score 457
E value 1.0e-45
Match length 112
% identity 81

NCBI Description heat shock protein 70 - rice (fragment)
>gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No. 236346
 Seq. ID uC-gsflnu33B059f09b1
 Method BLASTX
 NCBI GI g1345642
 BLAST score 250
 E value 1.0e-21
 Match length 64
 % identity 78
 NCBI Description FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450 75A1) (CYPLXXVA1) >gi_629710_pir_S38985 flavonoid 3',5'-hydroxylase Hfl - garden petunia >gi_311656_emb_CAA80266_ (Z22545) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_1853972_dbj_BAA03438_ (D14588) flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi_3426337 (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida] >gi_738772_prf_2001426B flavonoid 3',5'-hydroxylase [Petunia x hybrida]

Seq. No. 236347
 Seq. ID uC-gsflnu33B059f10b1
 Method BLASTX
 NCBI GI g127041
 BLAST score 283
 E value 3.0e-25
 Match length 53
 % identity 92
 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) ~ >gi_81647_pir_JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 236348
 Seq. ID uC-gsflnu33B059g03b1
 Method BLASTX
 NCBI GI g872116
 BLAST score 341
 E value 3.0e-32
 Match length 74
 % identity 46
 NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

Seq. No. 236349
 Seq. ID uC-gsflnu33B059g04b1
 Method BLASTX
 NCBI GI g3668089
 BLAST score 474
 E value 1.0e-47
 Match length 134
 % identity 67
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 236350
 Seq. ID uC-gsflnu33B060a08b1
 Method BLASTX
 NCBI GI g4063748

% identity 75
NCBI Description (AL035440) Avr9 elicitor response like protein [Arabidopsis thaliana]

Seq. No. 236356
Seq. ID uC-gsflnu33B060f12b1
Method BLASTX
NCBI GI g167367
BLAST score 227
E value 7.0e-19
Match length 44
% identity 100
NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 236357
Seq. ID uC-gsflnu33B060g10b1
Method BLASTX
NCBI GI g4105696
BLAST score 576
E value 1.0e-59
Match length 116
% identity 93
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No. 236358
Seq. ID uC-gsflnu33B060h07b1
Method BLASTX
NCBI GI g130972
BLAST score 138
E value 7.0e-09
Match length 61
% identity 49
NCBI Description PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
>gi_99952_pir_S10186 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - soybean >gi_18724_emb_CAA34401_ (X16352)
pyrroline-5-carboxylate reductase (AA 1- 274) [Glycine max]

Seq. No. 236359
Seq. ID uC-gsflnu33B061a07b1
Method BLASTX
NCBI GI g1915974
BLAST score 254
E value 3.0e-22
Match length 58
% identity 84
NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >gi_2102693
(U64818) fructokinase [Lycopersicon esculentum]

Seq. No. 236360
Seq. ID uC-gsflnu33B061b12b1
Method BLASTX
NCBI GI g135915
BLAST score 224
E value 1.0e-18
Match length 76
% identity 58
NCBI Description PATHOGENESIS-RELATED PROTEIN 5 PRECURSOR (PR-5)

Match length 104
 % identity 53
 NCBI Description (AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No. 236371
 Seq. ID uC-gsflnu33B062a11b1
 Method BLASTX
 NCBI GI g3941480
 BLAST score 361
 E value 6.0e-35
 Match length 71
 % identity 93
 NCBI Description (AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No. 236372
 Seq. ID uC-gsflnu33B062b02b1
 Method BLASTX
 NCBI GI g2583110
 BLAST score 162
 E value 4.0e-11
 Match length 62
 % identity 60
 NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]

Seq. No. 236373
 Seq. ID uC-gsflnu33B062b07b1
 Method BLASTX
 NCBI GI g4539292
 BLAST score 337
 E value 7.0e-32
 Match length 71
 % identity 86
 NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 236374
 Seq. ID uC-gsflnu33B062b10b1
 Method BLASTX
 NCBI GI g544075
 BLAST score 304
 E value 1.0e-42
 Match length 111
 % identity 53
 NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi_486768_pir_S35312 coatomer complex chain beta' - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop [Bos taurus]

Seq. No. 236375
 Seq. ID uC-gsflnu33B062c12b1
 Method BLASTX
 NCBI GI g860712
 BLAST score 193
 E value 6.0e-30
 Match length 86

% identity 70
 NCBI Description (U28735) coded for by C. elegans cDNA cm06e4; coded for by C. elegans cDNA CEESP39F; coded for by C. elegans cDNA CEESR26F; coded for by C. elegans cDNA CEESX83F; coded for by C. elegans cDNA yk16e9.3; coded for by C. elegans cDNA yk16e9.5; c

Seq. No. 236376
 Seq. ID uC-gsflnu33B062d01b1
 Method BLASTX
 NCBI GI g3415126
 BLAST score 181
 E value 1.0e-13
 Match length 91
 % identity 41
 NCBI Description (AF081678) phenylcoumaran benzylic ether reductase [Pinus taeda]

Seq. No. 236377
 Seq. ID uC-gsflnu33B062e01b1
 Method BLASTX
 NCBI GI g1050849
 BLAST score 204
 E value 4.0e-16
 Match length 110
 % identity 40
 NCBI Description (X83742) MAP kinase phosphatase [Xenopus laevis]

Seq. No. 236378
 Seq. ID uC-gsflnu33B062f02b1
 Method BLASTX
 NCBI GI g4263522
 BLAST score 261
 E value 6.0e-23
 Match length 97
 % identity 25
 NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236379
 Seq. ID uC-gsflnu33B062f04b1
 Method BLASTX
 NCBI GI g2369714
 BLAST score 143
 E value 5.0e-09
 Match length 36
 % identity 81
 NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 236380
 Seq. ID uC-gsflnu33B062h01b1
 Method BLASTX
 NCBI GI g3005576
 BLAST score 176
 E value 7.0e-28
 Match length 89
 % identity 69
 NCBI Description (AF047718) putative high affinity nitrate transporter;

09584016-101000

GmNRT2 [Glycine max]

Seq. No. 236381
 Seq. ID uC-gsflnu33B062h07b1
 Method BLASTX
 NCBI GI g4559380
 BLAST score 349
 E value 3.0e-33
 Match length 99
 % identity 63
 NCBI Description (AC006526) putative auxin-responsive GH3 protein
 [Arabidopsis thaliana]

Seq. No. 236382
 Seq. ID uC-gsflnu33B063a04b1
 Method BLASTX
 NCBI GI g3152585
 BLAST score 224
 E value 2.0e-18
 Match length 97
 % identity 55
 NCBI Description (AC002986) Contains similarity to auxin-induced protein
 TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis
 thaliana]

Seq. No. 236383
 Seq. ID uC-gsflnu33B063b10b1
 Method BLASTX
 NCBI GI g3250675
 BLAST score 368
 E value 9.0e-42
 Match length 124
 % identity 65
 NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 236384
 Seq. ID uC-gsflnu33B063c05b1
 Method BLASTX
 NCBI GI g1174199
 BLAST score 189
 E value 3.0e-14
 Match length 76
 % identity 55
 NCBI Description (U44760) S25-PR6 [Nicotiana tabacum]

Seq. No. 236385
 Seq. ID uC-gsflnu33B063e03b1
 Method BLASTX
 NCBI GI g1402912
 BLAST score 470
 E value 4.0e-47
 Match length 121
 % identity 74
 NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 236386
 Seq. ID uC-gsflnu33B063f11b1

Method BLASTX
 NCBI GI g4454025
 BLAST score 327
 E value 2.0e-30
 Match length 125
 % identity 48
 NCBI Description (AL035394) putative cellulase [Arabidopsis thaliana]

Seq. No. 236387
 Seq. ID uC-gsflnu33B063f12b1
 Method BLASTX
 NCBI GI g4522005
 BLAST score 180
 E value 4.0e-13
 Match length 136
 % identity 33
 NCBI Description (AC007069) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 236388
 Seq. ID uC-gsflnu33B063g02b1
 Method BLASTX
 NCBI GI g4097579
 BLAST score 257
 E value 2.0e-22
 Match length 72
 % identity 68
 NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 236389
 Seq. ID uC-gsflnu33B063g10b1
 Method BLASTX
 NCBI GI g4115377
 BLAST score 203
 E value 6.0e-16
 Match length 46
 % identity 80
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 236390
 Seq. ID uC-gsflnu33B063h02b1
 Method BLASTX
 NCBI GI g166410
 BLAST score 164
 E value 3.0e-19
 Match length 64
 % identity 69
 NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 236391
 Seq. ID uC-gsflnu33B063h03b1
 Method BLASTX
 NCBI GI g4263517
 BLAST score 146
 E value 1.0e-12
 Match length 63
 % identity 54

NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]

Seq. No. 236392
Seq. ID uC-gsflnu33B064b01b1
Method BLASTX
NCBI GI g3805956
BLAST score 266
E value 3.0e-29
Match length 72
% identity 89
NCBI Description (Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No. 236393
Seq. ID uC-gsflnu33B064b09b1
Method BLASTX
NCBI GI g2980795
BLAST score 262
E value 4.0e-23
Match length 86
% identity 58
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 236394
Seq. ID uC-gsflnu33B064c01b1
Method BLASTX
NCBI GI g2459440
BLAST score 434
E value 5.0e-43
Match length 129
% identity 64
NCBI Description (AC002332) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 236395
Seq. ID uC-gsflnu33B064d12b1
Method BLASTX
NCBI GI g4371285
BLAST score 194
E value 6.0e-15
Match length 95
% identity 48
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236396
Seq. ID uC-gsflnu33B064e01b1
Method BLASTX
NCBI GI g3249105
BLAST score 237
E value 2.0e-20
Match length 68
% identity 69
NCBI Description (AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 236397

Method BLASTX
 NCBI GI g4512670
 BLAST score 216
 E value 2.0e-17
 Match length 77
 % identity 44
 NCBI Description (AC006931) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 236408
 Seq. ID uC-gsflnu33B066e05b1
 Method BLASTX
 NCBI GI g2398523
 BLAST score 220
 E value 6.0e-18
 Match length 88
 % identity 61
 NCBI Description (Y13721) Transcription factor [Arabidopsis thaliana]

Seq. No. 236409
 Seq. ID uC-gsflnu33B066f02b1
 Method BLASTX
 NCBI GI g3355780
 BLAST score 150
 E value 8.0e-10
 Match length 28
 % identity 86
 NCBI Description (AJ004997) expansin18 [Lycopersicon esculentum]

Seq. No. 236410
 Seq. ID uC-gsflnu33B066f08b1
 Method BLASTX
 NCBI GI g2522227
 BLAST score 149
 E value 2.0e-09
 Match length 79
 % identity 43
 NCBI Description (AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]

Seq. No. 236411
 Seq. ID uC-gsflnu33B066g12b1
 Method BLASTX
 NCBI GI g4539292
 BLAST score 452
 E value 4.0e-45
 Match length 96
 % identity 86
 NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 236412
 Seq. ID uC-gsflnu33B066h01b1
 Method BLASTX
 NCBI GI g3947719
 BLAST score 249
 E value 3.0e-21
 Match length 53

E value 1.0e-09
 Match length 47
 % identity 55
 NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No. 236418
 Seq. ID uC-gsflnu33B068g09b1
 Method BLASTX
 NCBI GI g2564249
 BLAST score 208
 E value 2.0e-16
 Match length 84
 % identity 50
 NCBI Description (Y08686) serine palmitoyltransferase, subunit II [Homo sapiens] >gi_3043576_dbj_BAA25452_ (AB011098) KIAA0526 protein [Homo sapiens] >gi_4186182 (AF1111168) serine palmitoyl transferase, subunit II [Homo sapiens]

Seq. No. 236419
 Seq. ID uC-gsflnu33B070c07b1
 Method BLASTX
 NCBI GI g3063442
 BLAST score 180
 E value 3.0e-13
 Match length 77
 % identity 52
 NCBI Description (AC003981) F22013.6 [Arabidopsis thaliana]

Seq. No. 236420
 Seq. ID uC-gsflnu33B070d10b1
 Method BLASTX
 NCBI GI g464863
 BLAST score 303
 E value 3.0e-28
 Match length 65
 % identity 94
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING PROTEIN HOMOLOG 10) >gi_422297_pir_JN0610 probable transcription factor DdTBP10 - slime mold (Dictyostelium discoideum) (fragment) >gi_290057 (L16579) HIV1 TAT-binding protein [Dictyostelium discoideum]

Seq. No. 236421
 Seq. ID uC-gsflnu33B070f12b1
 Method BLASTX
 NCBI GI g3980407
 BLAST score 192
 E value 9.0e-23
 Match length 122
 % identity 48
 NCBI Description (AC004561) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 236422

E value 4.0e-15
 Match length 38
 % identity 84
 NCBI Description (U71244) pathogenesis-related group 5 protein [Brassica rapa]

Seq. No. 236439
 Seq. ID uC-gsflnu33B073c07b1
 Method BLASTX
 NCBI GI g4193388
 BLAST score 210
 E value 2.0e-17
 Match length 45
 % identity 89
 NCBI Description (AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No. 236440
 Seq. ID uC-gsflnu33B073f06b1
 Method BLASTX
 NCBI GI g4531434
 BLAST score 160
 E value 2.0e-11
 Match length 40
 % identity 70
 NCBI Description (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No. 236441
 Seq. ID uC-gsflnu33B074d05b1
 Method BLASTX
 NCBI GI g2129597
 BLAST score 457
 E value 9.0e-46
 Match length 93
 % identity 92
 NCBI Description glutamate dehydrogenase 1 - Arabidopsis thaliana
 >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No. 236442
 Seq. ID uC-gsflnu33B074d11b1
 Method BLASTX
 NCBI GI g4432855
 BLAST score 197
 E value 2.0e-15
 Match length 102
 % identity 50
 NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 236443
 Seq. ID uC-gsflnu33B074e06b1
 Method BLASTX
 NCBI GI g2708743
 BLAST score 144
 E value 6.0e-09
 Match length 139

% identity 26
 NCBI Description (AC003952) putative Tal-1-like reverse transcriptase
 [Arabidopsis thaliana]

Seq. No. 236444
 Seq. ID uC-gsflnu33B074e07b1
 Method BLASTX
 NCBI GI g4539452
 BLAST score 518
 E value 6.0e-53
 Match length 119
 % identity 75
 NCBI Description (AL049500) putative phosphoribosylanthranilate transferase
 [Arabidopsis thaliana]

Seq. No. 236445
 Seq. ID uC-gsflnu33B074g03b1
 Method BLASTX
 NCBI GI g2842478
 BLAST score 356
 E value 5.0e-34
 Match length 112
 % identity 65
 NCBI Description (AL021749) receptor protein kinase like protein
 [Arabidopsis thaliana]

Seq. No. 236446
 Seq. ID uC-gsflnu33B074h01b1
 Method BLASTX
 NCBI GI g553111
 BLAST score 146
 E value 2.0e-09
 Match length 112
 % identity 24
 NCBI Description (J03625) hydroproline-rich protein [Glycine max]

Seq. No. 236447
 Seq. ID uC-gsflnu33B074h03b1
 Method BLASTX
 NCBI GI g1666236
 BLAST score 233
 E value 2.0e-19
 Match length 117
 % identity 38
 NCBI Description (U76261) unknown [Hordeum vulgare]

Seq. No. 236448
 Seq. ID uC-gsflnu33B074h05b1
 Method BLASTX
 NCBI GI g2618698
 BLAST score 319
 E value 1.0e-29
 Match length 124
 % identity 53
 NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 236449

Seq. ID uC-gsflnu33B074h07b1
 Method BLASTX
 NCBI GI g3695059
 BLAST score 283
 E value 3.0e-25
 Match length 81
 % identity 73
 NCBI Description (AF064787) rac GTPase activating protein 1 [Lotus japonicus]

Seq. No. 236450
 Seq. ID uC-gsflnu33B074h12b1
 Method BLASTX
 NCBI GI g2760835
 BLAST score 622
 E value 5.0e-65
 Match length 148
 % identity 80
 NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

Seq. No. 236451
 Seq. ID uC-gsflnu33B075b03b1
 Method BLASTX
 NCBI GI g1707955
 BLAST score 477
 E value 4.0e-48
 Match length 96
 % identity 92
 NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1 (GLUTAMATE--AMMONIA LIGASE) >gi_1134896_emb_CAA63981_ (X94320) glutamine synthetase [Vitis vinifera]

Seq. No. 236452
 Seq. ID uC-gsflnu33B075b04b1
 Method BLASTX
 NCBI GI g1361983
 BLAST score 365
 E value 4.0e-35
 Match length 105
 % identity 70
 NCBI Description ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No. 236453
 Seq. ID uC-gsflnu33B075c06b1
 Method BLASTX
 NCBI GI g3142296
 BLAST score 252
 E value 6.0e-22
 Match length 86
 % identity 56
 NCBI Description (AC002411) Contains similarity to hypothetical mitochondrial import receptor subunit gb_298597 from S. pombe. ESTs gb_T45575 and gb_Z26435 and gb_AA394576 come from this gene. [Arabidopsis thaliana]

Seq. No. 236454

NCBI GI g2642428
 BLAST score 298
 E value 5.0e-27
 Match length 118
 % identity 48
 NCBI Description (AC002391) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No. 236460
 Seq. ID uC-gsflnu33B075g04b1
 Method BLASTX
 NCBI GI g2454629
 BLAST score 272
 E value 1.0e-24
 Match length 62
 % identity 82
 NCBI Description (AF019559) cytosolic glutamine synthetase; GS1 [Daucus carota]

Seq. No. 236461
 Seq. ID uC-gsflnu33B075g09b1
 Method BLASTX
 NCBI GI g4539437
 BLAST score 195
 E value 5.0e-15
 Match length 42
 % identity 83
 NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 236462
 Seq. ID uC-gsflnu33B075h04b1
 Method BLASTX
 NCBI GI g3250680
 BLAST score 513
 E value 3.0e-52
 Match length 121
 % identity 82
 NCBI Description (AL024486) aspartate kinase-homoserine dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No. 236463
 Seq. ID uC-gsflnu33B076e06b1
 Method BLASTX
 NCBI GI g1408471
 BLAST score 181
 E value 3.0e-13
 Match length 40
 % identity 88
 NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No. 236464
 Seq. ID uC-gsflnu33B076e12b1
 Method BLASTX
 NCBI GI g3132475
 BLAST score 176

BLAST score 266
 E value 2.0e-23
 Match length 106
 % identity 53
 NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 236480
 Seq. ID uC-gsflnu33B078h10b1
 Method BLASTX
 NCBI GI g3559811
 BLAST score 246
 E value 7.0e-21
 Match length 60
 % identity 78
 NCBI Description (AJ010735) gr1-protein [Arabidopsis thaliana]

Seq. No. 236481
 Seq. ID uC-gsflnu33B079d01b1
 Method BLASTX
 NCBI GI g2586123
 BLAST score 463
 E value 2.0e-46
 Match length 100
 % identity 87
 NCBI Description (U89511) b-keto acyl reductase [Allium porrum]

Seq. No. 236482
 Seq. ID uC-gsflnu33B079d05b1
 Method BLASTX
 NCBI GI g4580461
 BLAST score 286
 E value 3.0e-26
 Match length 59
 % identity 92
 NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 236483
 Seq. ID uC-gsflnu33B079e06b1
 Method BLASTX
 NCBI GI g117188
 BLAST score 411
 E value 2.0e-40
 Match length 127
 % identity 57
 NCBI Description CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2)
 >gi_81423_pir__A35867 cytochrome P450 71A1 - avocado

Seq. No. 236484
 Seq. ID uC-gsflnu33B079f03b1
 Method BLASTX
 NCBI GI g123554
 BLAST score 142
 E value 3.0e-09
 Match length 33
 % identity 79
 NCBI Description 18.1 KD CLASS I HEAT SHOCK PROTEIN >gi_99978_pir_S16248
 heat shock protein 18 (clone pMsHsp18.1) - alfalfa

NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana].

Seq. No. 236490
 Seq. ID uC-gsflnu33B081e05b1
 Method BLASTX
 NCBI GI g2649749
 BLAST score 160
 E value 9.0e-11
 Match length 131
 % identity 36

NCBI Description (AE001045) proliferating-cell nucleolar antigen P120, putative [Archaeoglobus fulgidus]

Seq. No. 236491
 Seq. ID uC-gsflnu33B081f10b1
 Method BLASTX
 NCBI GI g4204278
 BLAST score 179
 E value 4.0e-13
 Match length 122
 % identity 35

NCBI Description (AC004146) putative Cytochrome P450 protein [Arabidopsis thaliana].

Seq. No. 236492
 Seq. ID uC-gsflnu33B081g08b1
 Method BLASTX
 NCBI GI g3080416
 BLAST score 215
 E value 3.0e-17
 Match length 53
 % identity 83

NCBI Description (AL022604) UDP-galactose transporter - like protein [Arabidopsis thaliana]

Seq. No. 236493
 Seq. ID uC-gsflnu33B081h05b1
 Method BLASTX
 NCBI GI g4115383
 BLAST score 168
 E value 3.0e-12
 Match length 71
 % identity 45

NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 236494
 Seq. ID uC-gsflnu33B082a08b1
 Method BLASTX
 NCBI GI g416641
 BLAST score 253
 E value 1.0e-21
 Match length 52
 % identity 85

NCBI Description INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4
 >gi_287568_dbj_BAA03309_ (D14413) ORF [Vigna radiata]

Seq. No. 236495
 Seq. ID uC-gsflnu33B082a11b1
 Method BLASTX
 NCBI GI g1076387
 BLAST score 338
 E value 8.0e-32
 Match length 89
 % identity 69
 NCBI Description protein kinase homolog - Arabidopsis thaliana
 >gi_717180_emb_CAA55866_(X79279) protein kinase homologous
 to shaggy and glycogen synthase kinase-3 [Arabidopsis
 thaliana]

Seq. No. 236496
 Seq. ID uC-gsflnu33B082c08b1
 Method BLASTX
 NCBI GI g1755166
 BLAST score 381
 E value 9.0e-37
 Match length 102
 % identity 74
 NCBI Description (U75194) germin-like protein [Arabidopsis thaliana]

Seq. No. 236497
 Seq. ID uC-gsflnu33B082d11b1
 Method BLASTX
 NCBI GI g1171579
 BLAST score 386
 E value 1.0e-46
 Match length 129
 % identity 71
 NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 236498
 Seq. ID uC-gsflnu33B082e10b1
 Method BLASTX
 NCBI GI g3337361
 BLAST score 431
 E value 8.0e-43
 Match length 99
 % identity 79
 NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 236499
 Seq. ID uC-gsflnu33B082f11b1
 Method BLASTX
 NCBI GI g4220527
 BLAST score 611
 E value 1.0e-63
 Match length 131
 % identity 82
 NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 236500
 Seq. ID uC-gsflnu33B082g10b1
 Method BLASTX
 NCBI GI g2827548

BLAST score 222
 E value 5.0e-28
 Match length 137
 % identity 50
 NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No. 236501
 Seq. ID uC-gsflnu33B082g11b1
 Method BLASTX
 NCBI GI g1749596
 BLAST score 169
 E value 8.0e-12
 Match length 42
 % identity 69
 NCBI Description (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT Accession Number P16638 [Schizosaccharomyces pombe]

Seq. No. 236502
 Seq. ID uC-gsflnu33B082h02b1
 Method BLASTX
 NCBI GI g4539350
 BLAST score 266
 E value 3.0e-38
 Match length 113
 % identity 71
 NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 236503
 Seq. ID uC-gsflnu33B083a02b1
 Method BLASTX
 NCBI GI g4337189
 BLAST score 237
 E value 6.0e-20
 Match length 74
 % identity 55
 NCBI Description (AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No. 236504
 Seq. ID uC-gsflnu33B083a04b1
 Method BLASTX
 NCBI GI g2842477
 BLAST score 237
 E value 4.0e-20
 Match length 72
 % identity 65
 NCBI Description (AL021749) copper-binding protein-like [Arabidopsis thaliana]

Seq. No. 236505
 Seq. ID uC-gsflnu33B083b03b1
 Method BLASTX
 NCBI GI g1076708
 BLAST score 375
 E value 4.0e-36
 Match length 75

E value 4.0e-13
 Match length 60
 % identity 52
 NCBI Description (Z97341) limonene cyclase [Arabidopsis thaliana]

Seq. No. 236511
 Seq. ID uC-gsflnu33B084c10b1
 Method BLASTX
 NCBI GI g730645
 BLAST score 516
 E value 1.0e-52
 Match length 111
 % identity 90
 NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir_S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No. 236512
 Seq. ID uC-gsflnu33B084d03b1
 Method BLASTX
 NCBI GI g4218011
 BLAST score 150
 E value 1.0e-09
 Match length 53
 % identity 58
 NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 236513
 Seq. ID uC-gsflnu33B084e03b1
 Method BLASTX
 NCBI GI g2739381
 BLAST score 339
 E value 7.0e-32
 Match length 112
 % identity 60
 NCBI Description (AC002505) putative patatin [Arabidopsis thaliana]

Seq. No. 236514
 Seq. ID uC-gsflnu33B084e11b1
 Method BLASTX
 NCBI GI g2618684
 BLAST score 309
 E value 3.0e-28
 Match length 95
 % identity 62
 NCBI Description (AC002510) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase [Arabidopsis thaliana] >gi_3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate

00684016-101000

09584015-101000

N-acetylglucosaminephosphotransferase [Arabidopsis thaliana]

Seq. No. 236515
 Seq. ID uC-gsflnu33B084f05b1
 Method BLASTX
 NCBI GI g4415938
 BLAST score 192
 E value 4.0e-27
 Match length 83
 % identity 72
 NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

Seq. No. 236516
 Seq. ID uC-gsflnu33B084f09b1
 Method BLASTX
 NCBI GI g3759177
 BLAST score 161
 E value 6.0e-11
 Match length 47
 % identity 72
 NCBI Description (AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807_ (AB018409) 3-phosphoserine phosphatase [Arabidopsis thaliana]

Seq. No. 236517
 Seq. ID uC-gsflnu33B084h06b1
 Method BLASTX
 NCBI GI g3252815
 BLAST score 290
 E value 4.0e-26
 Match length 74
 % identity 78
 NCBI Description (AC004705) vacuolar sorting receptor-like protein [Arabidopsis thaliana] >gi_3810588 (AC005398) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No. 236518
 Seq. ID uC-gsflnu33B085d05b1
 Method BLASTX
 NCBI GI g4580461
 BLAST score 286
 E value 3.0e-26
 Match length 59
 % identity 92
 NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 236519
 Seq. ID uC-gsflnu33B085h03b1
 Method BLASTX
 NCBI GI g3080447
 BLAST score 161
 E value 5.0e-20
 Match length 117
 % identity 54
 NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 236520
 Seq. ID uC-gsflnu33B085h07b1
 Method BLASTX
 NCBI GI g3935168
 BLAST score 250
 E value 2.0e-21
 Match length 96
 % identity 58
 NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 236521
 Seq. ID uC-gsflnu33B088a02b1
 Method BLASTX
 NCBI GI g3176684
 BLAST score 360
 E value 2.0e-34
 Match length 107
 % identity 67
 NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317, gb_T20785, gb_AA586285 and gb_AA712578 come from this gene. [Arabidopsis thaliana]

Seq. No. 236522
 Seq. ID uC-gsflnu33B088a05b1
 Method BLASTX
 NCBI GI g3540219
 BLAST score 187
 E value 2.0e-14
 Match length 52
 % identity 62
 NCBI Description (D87686) KIAA0017 protein [Homo sapiens]

Seq. No. 236523
 Seq. ID uC-gsflnu33B088b05b1
 Method BLASTX
 NCBI GI g1946279
 BLAST score 287
 E value 7.0e-26
 Match length 102
 % identity 47
 NCBI Description (Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]

Seq. No. 236524
 Seq. ID uC-gsflnu33B088b11b1
 Method BLASTX
 NCBI GI g3915601
 BLAST score 257
 E value 1.0e-22
 Match length 78
 % identity 63
 NCBI Description ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (A1 38 KD SUBUNIT) (RF-C 38 KD SUBUNIT) (RFC38) >gi_1498259 (L07541) replication factor C, 38-kDa subunit [Homo sapiens] >gi_4506489_ref_NP_002906.1_pRFC3_ replication factor C (activator 1) 3 (38kD)

Seq. No. 236525
 Seq. ID uC-gsflnu33B088c02b1
 Method BLASTX
 NCBI GI g407942
 BLAST score 218
 E value 1.0e-17
 Match length 53
 % identity 70
 NCBI Description (U02496) epoxide hydrolase [Solanum tuberosum]

Seq. No. 236526
 Seq. ID uC-gsflnu33B088d05b1
 Method BLASTX
 NCBI GI g3461820
 BLAST score 270
 E value 2.0e-24
 Match length 60
 % identity 73
 NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 236527
 Seq. ID uC-gsflnu33B088d06b1
 Method BLASTX
 NCBI GI g3702321
 BLAST score 447
 E value 9.0e-45
 Match length 98
 % identity 50
 NCBI Description (AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No. 236528
 Seq. ID uC-gsflnu33B088e10b1
 Method BLASTX
 NCBI GI g3757515
 BLAST score 189
 E value 2.0e-14
 Match length 66
 % identity 59
 NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236529
 Seq. ID uC-gsflnu33B088e12b1
 Method BLASTX
 NCBI GI g231757
 BLAST score 625
 E value 3.0e-65
 Match length 146
 % identity 84
 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
 (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
 3-O-METHYLTRANSFERASE) (COMT) >gi_99653_pir_S18568
 lignin-bispecific O-methyltransferase (EC 2.1.1.-) -
 quaking aspen >gi_20951_emb_CAA44006_(X62096) lignin
 bispecific acid/5-hydroxyferulic acid methyltransferase
 [Populus tremuloides] >gi_2226267 (U13171) caffeic

09684015-101000

acid/5-hydroxyferulic acid O-methyltransferase [Populus tremuloides]

Seq. No. 236530
Seq. ID uC-gsflnu33B088f07b1
Method BLASTX
NCBI GI g3135274
BLAST score 196
E value 3.0e-15
Match length 45
% identity 82
NCBI Description (AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No. 236531
Seq. ID uC-gsflnu33B088f08b1
Method BLASTX
NCBI GI g3600048
BLAST score 409
E value 5.0e-45
Match length 115
% identity 77
NCBI Description (AF080120) similar to hypothetical proteins in Schizosaccharomyces pombe (GB:Z98533) and C. elegans (GB:Z48334 and Z78419) [Arabidopsis thaliana]

Seq. No. 236532
Seq. ID uC-gsflnu33B088g07b1
Method BLASTX
NCBI GI g3643604
BLAST score 225
E value 8.0e-19
Match length 81
% identity 56
NCBI Description (AC005395) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 236533
Seq. ID uC-gsflnu33B088h03b1
Method BLASTX
NCBI GI g3702334
BLAST score 185
E value 7.0e-14
Match length 116
% identity 41
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236534
Seq. ID uC-gsflnu33B088h04b1
Method BLASTX
NCBI GI g4193382
BLAST score 392
E value 4.0e-38
Match length 86
% identity 84
NCBI Description (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
>gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis

thaliana]

Seq. No. 236535
 Seq. ID uC-gsflnu33B089a12b1
 Method BLASTX
 NCBI GI g4455190
 BLAST score 266
 E value 2.0e-23
 Match length 69
 % identity 80
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 236536
 Seq. ID uC-gsflnu33B089b01b1
 Method BLASTX
 NCBI GI g3746060
 BLAST score 463
 E value 2.0e-46
 Match length 116
 % identity 78
 NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 236537
 Seq. ID uC-gsflnu33B089b04b1
 Method BLASTX
 NCBI GI g2465923
 BLAST score 181
 E value 7.0e-14
 Match length 47
 % identity 68
 NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 236538
 Seq. ID uC-gsflnu33B089b06b1
 Method BLASTX
 NCBI GI g1762939
 BLAST score 136
 E value 1.0e-08
 Match length 35
 % identity 69
 NCBI Description (U66266) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No. 236539
 Seq. ID uC-gsflnu33B089b09b1
 Method BLASTX
 NCBI GI g3080452
 BLAST score 321
 E value 4.0e-30
 Match length 88
 % identity 67
 NCBI Description (AL022605) putative L-ascorbate oxidase [Arabidopsis thaliana]

Seq. No. 236540
 Seq. ID uC-gsflnu33B089c05b1

Method BLASTX
 NCBI GI g1169782
 BLAST score 506
 E value 1.0e-51
 Match length 112
 % identity 88
 NCBI Description FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No. 236541
 Seq. ID uC-gsflnu33B089c12b1
 Method BLASTX
 NCBI GI g3935148
 BLAST score 190
 E value 2.0e-14
 Match length 57
 % identity 68
 NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No. 236542
 Seq. ID uC-gsflnu33B089d05b1
 Method BLASTX
 NCBI GI g3212863
 BLAST score 182
 E value 5.0e-14
 Match length 42
 % identity 83
 NCBI Description (AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No. 236543
 Seq. ID uC-gsflnu33B089d12b1
 Method BLASTX
 NCBI GI g130181
 BLAST score 180
 E value 2.0e-13
 Match length 37
 % identity 86
 NCBI Description PHYTOCHROME A TYPE 3 (AP3) >gi_82335_pir_S00096
 phytochrome 3 - oat >gi_16111_emb_CAA26999_ (X03242)
 phytochrome type 3 (aa 1-1129) [Avena sativa]

Seq. No. 236544
 Seq. ID uC-gsflnu33B089e04b1
 Method BLASTX
 NCBI GI g1663722
 BLAST score 321
 E value 6.0e-30
 Match length 81
 % identity 70
 NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 236545
 Seq. ID uC-gsflnu33B089f04b1
 Method BLASTX
 NCBI GI g167367
 BLAST score 153

E value 1.0e-10
Match length 49
% identity 61
NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 236546
Seq. ID uC-gsflnu33B089g03b1
Method BLASTX
NCBI GI g2642215
BLAST score 136
E value 1.0e-08
Match length 24
% identity 100
NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]

Seq. No. 236547
Seq. ID uC-gsflnu33B089h12b1
Method BLASTX
NCBI GI g3241943
BLAST score 140
E value 1.0e-08
Match length 34
% identity 76
NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236548
Seq. ID uC-gsflnu33B090a07b1
Method BLASTX
NCBI GI g3292816
BLAST score 580
E value 4.0e-60
Match length 134
% identity 33
NCBI Description (AL031018) putative fizzy-related protein [Arabidopsis thaliana]

Seq. No. 236549
Seq. ID uC-gsflnu33B090b08b1
Method BLASTX
NCBI GI g2129677
BLAST score 170
E value 1.0e-12
Match length 45
% identity 67
NCBI Description probable1 N-acetyltransferase hookless 1 - Arabidopsis thaliana >gi_1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_4468983_emb_CAB38297_ (AL035605) probable N-acetyltransferase hookless 1 [Arabidopsis thaliana]

Seq. No. 236550
Seq. ID uC-gsflnu33B090b12b1
Method BLASTX
NCBI GI g3355468
BLAST score 150
E value 3.0e-10

Seq. ID uC-gsflnu33B090h04b1
 Method BLASTX
 NCBI GI g4389417
 BLAST score 509
 E value 6.0e-52
 Match length 105
 % identity 87
 NCBI Description (AF055369) nitrate reductase [Glycine max]

Seq. No. 236562
 Seq. ID uC-gsflnu33B090h10b1
 Method BLASTX
 NCBI GI g4468990
 BLAST score 138
 E value 7.0e-09
 Match length 53
 % identity 58
 NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 236563
 Seq. ID uC-gsflnu33B090h11b1
 Method BLASTX
 NCBI GI g2760837
 BLAST score 256
 E value 4.0e-22
 Match length 129
 % identity 40
 NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 236564
 Seq. ID uC-gsflnu33B091b03b1
 Method BLASTX
 NCBI GI g2245132
 BLAST score 279
 E value 8.0e-25
 Match length 77
 % identity 70
 NCBI Description (Z97344) syntaxin [Arabidopsis thaliana]

Seq. No. 236565
 Seq. ID uC-gsflnu33B091b11b1
 Method BLASTX
 NCBI GI g3582260
 BLAST score 354
 E value 9.0e-34
 Match length 82
 % identity 84
 NCBI Description (M27221) lysyl-tRNA synthetase [Sinorhizobium meliloti]

Seq. No. 236566
 Seq. ID uC-gsflnu33B091c07b1
 Method BLASTX
 NCBI GI g1345132
 BLAST score 289
 E value 2.0e-26
 Match length 60
 % identity 93

Match length 73
 % identity 62
 NCBI Description (AC006587) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 236572
 Seq. ID uC-gsflnu33B092a06b1
 Method BLASTX
 NCBI GI g602292
 BLAST score 442
 E value 6.0e-44
 Match length 104
 % identity 84
 NCBI Description (U17987) RCH2 protein [Brassica napus]

Seq. No. 236573
 Seq. ID uC-gsflnu33B092b01b1
 Method BLASTX
 NCBI GI g861366
 BLAST score 359
 E value 4.0e-34
 Match length 125
 % identity 57
 NCBI Description (U28991) coded for by C. elegans cDNA cm21c7 [Caenorhabditis elegans]

Seq. No. 236574
 Seq. ID uC-gsflnu33B092b10b1
 Method BLASTX
 NCBI GI g3024127
 BLAST score 369
 E value 1.0e-35
 Match length 91
 % identity 77
 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
 >gi_1655578_emb_CAA95857_(Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]

Seq. No. 236575
 Seq. ID uC-gsflnu33B092c08b1
 Method BLASTX
 NCBI GI g549750
 BLAST score 148
 E value 2.0e-09
 Match length 116
 % identity 34
 NCBI Description HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
 >gi_539221_pir_S38045 hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_(Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No. 236576
 Seq. ID uC-gsflnu33B092e07b1
 Method BLASTX
 NCBI GI g2245132
 BLAST score 153

E value 2.0e-10
Match length 42
% identity 71
NCBI Description (Z97344) syntaxin [Arabidopsis thaliana]

Seq. No. 236577
Seq. ID uC-gsflnu33B092f11b1
Method BLASTX
NCBI GI g2306917
BLAST score 239
E value 3.0e-36
Match length 85
% identity 93
NCBI Description (AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No. 236578
Seq. ID uC-gsflnu33B092g09b1
Method BLASTX
NCBI GI g3098571
BLAST score 236
E value 9.0e-20
Match length 134
% identity 37
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]

Seq. No. 236579
Seq. ID uC-gsflnu33B093b08b1
Method BLASTX
NCBI GI g3372233
BLAST score 134
E value 3.0e-12
Match length 70
% identity 60
NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana]

Seq. No. 236580
Seq. ID uC-gsflnu33B093b11b1
Method BLASTX
NCBI GI g4467135
BLAST score 395
E value 2.0e-38
Match length 130
% identity 60
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 236581
Seq. ID uC-gsflnu33B093c02b1
Method BLASTX
NCBI GI g2181190
BLAST score 152
E value 5.0e-10
Match length 99
% identity 37
NCBI Description (Y12531) serine/threonine kinase [Brassica oleracea]

Method BLASTX
 NCBI GI g4220472
 BLAST score 394
 E value 3.0e-38
 Match length 122
 % identity 58
 NCBI Description (AC006069) similar to yeast cccl protein [Arabidopsis thaliana]

Seq. No. 236588
 Seq. ID uC-gsflnu33B093d04b1
 Method BLASTX
 NCBI GI g1632831
 BLAST score 333
 E value 5.0e-31
 Match length 72
 % identity 92
 NCBI Description (Z49698) orf [Ricinus communis]

Seq. No. 236589
 Seq. ID uC-gsflnu33B093d10b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 1.0e-14
 Match length 47
 % identity 68
 NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No. 236590
 Seq. ID uC-gsflnu33B093e01b1
 Method BLASTX
 NCBI GI g3258570
 BLAST score 297
 E value 7.0e-27
 Match length 143
 % identity 46
 NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 236591
 Seq. ID uC-gsflnu33B093e08b1
 Method BLASTX
 NCBI GI g3850587
 BLAST score 258
 E value 3.0e-22
 Match length 144
 % identity 40
 NCBI Description (AC005278) Strong similarity to gi_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No. 236592
 Seq. ID uC-gsflnu33B093f12b1
 Method BLASTX
 NCBI GI g1346172
 BLAST score 284

E value 2.0e-25
 Match length 57
 % identity 91
 NCBI Description 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78)
 (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP)
 >gi_170384 (L08830) glucose-regulated protein 78
 [Lycopersicon esculentum]

Seq. No. 236593
 Seq. ID uC-gsflnu33B093g03b1
 Method BLASTX
 NCBI GI g3549681
 BLAST score 391
 E value 6.0e-38
 Match length 134
 % identity 57
 NCBI Description (AL031394) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No. 236594
 Seq. ID uC-gsflnu33B093h09b1
 Method BLASTX
 NCBI GI g1934730
 BLAST score 330
 E value 8.0e-31
 Match length 81
 % identity 79
 NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]

Seq. No. 236595
 Seq. ID uC-gsflnu33B094b01b1
 Method BLASTX
 NCBI GI g3033400
 BLAST score 293
 E value 1.0e-26
 Match length 86
 % identity 66
 NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 236596
 Seq. ID uC-gsflnu33B094b08b1
 Method BLASTX
 NCBI GI g2499015
 BLAST score 173
 E value 2.0e-12
 Match length 102
 % identity 36
 NCBI Description TRIGGER FACTOR (TF) >gi_1001378_dbj_BAA10868_ (D64006)
 trigger factor [Synechocystis sp.]

Seq. No. 236597
 Seq. ID uC-gsflnu33B094c07b1
 Method BLASTX
 NCBI GI g4220474
 BLAST score 252
 E value 9.0e-22

Match length 117
 % identity 50
 NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No. 236598
 Seq. ID uC-gsflnu33B094c11b1
 Method BLASTX
 NCBI GI g3819697
 BLAST score 197
 E value 2.0e-15
 Match length 100
 % identity 47
 NCBI Description (AJ009608) BnMAP4K alpha1 [Brassica napus]

Seq. No. 236599
 Seq. ID uC-gsflnu33B094f05b1
 Method BLASTX
 NCBI GI g4545262
 BLAST score 143
 E value 2.0e-09
 Match length 34
 % identity 85
 NCBI Description (AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No. 236600
 Seq. ID uC-gsflnu33B094g09b1
 Method BLASTX
 NCBI GI g3236240
 BLAST score 179
 E value 2.0e-13
 Match length 81
 % identity 49
 NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 236601
 Seq. ID uC-gsflnu33B094g10b1
 Method BLASTX
 NCBI GI g3702324
 BLAST score 149
 E value 1.0e-09
 Match length 107
 % identity 35
 NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236602
 Seq. ID uC-gsflnu33B094g12b1
 Method BLASTX
 NCBI GI g2290532
 BLAST score 238
 E value 3.0e-20
 Match length 53
 % identity 85
 NCBI Description (U94748) AN11 [Petunia x hybrida]

Seq. No. 236603

BLAST score 164
 E value 1.0e-11
 Match length 58
 % identity 55
 NCBI Description (AB009307) bpwl [Hordeum vulgare]

Seq. No. 236609
 Seq. ID uC-gsflnu33B097a12b1
 Method BLASTX
 NCBI GI g1352186
 BLAST score 368
 E value 2.0e-35
 Match length 118
 % identity 58
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 236610
 Seq. ID uC-gsflnu33B097c08b1
 Method BLASTX
 NCBI GI g1076746
 BLAST score 200
 E value 8.0e-16
 Match length 40
 % identity 93
 NCBI Description heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No. 236611
 Seq. ID uC-gsflnu33B098b10b1
 Method BLASTX
 NCBI GI g3319882
 BLAST score 303
 E value 3.0e-28
 Match length 65
 % identity 91
 NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No. 236612
 Seq. ID uC-gsflnu33B100b06b1
 Method BLASTX
 NCBI GI g973313
 BLAST score 346
 E value 4.0e-55
 Match length 117
 % identity 93
 NCBI Description (U30250) myo-inositol 1-phosphate synthase isozyme-2 [Arabidopsis thaliana]

Seq. No. 236613
 Seq. ID uC-gsflnu33B100b09b1
 Method BLASTX
 NCBI GI g421826
 BLAST score 431

E value 1.0e-42
 Match length 141
 % identity 63
 NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
 >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
 thaliana]

Seq. No. 236614
 Seq. ID uC-gsflnu33B100c01b1
 Method BLASTX
 NCBI GI g3522945
 BLAST score 138
 E value 3.0e-12
 Match length 110
 % identity 33
 NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 236615
 Seq. ID uC-gsflnu33B100d09b1
 Method BLASTX
 NCBI GI g4335754
 BLAST score 530
 E value 3.0e-54
 Match length 145
 % identity 68
 NCBI Description (AC006284) putative acid phosphatase (contains
 metallo-phosphoesterase motif, prosite: QDOC50185)
 [Arabidopsis thaliana]

Seq. No. 236616
 Seq. ID uC-gsflnu33B100e09b1
 Method BLASTX
 NCBI GI g3800952
 BLAST score 206
 E value 3.0e-16
 Match length 109
 % identity 47
 NCBI Description (AF100657) No definition line found [Caenorhabditis
 elegans]

Seq. No. 236617
 Seq. ID uC-gsflnu33B100g01b1
 Method BLASTX
 NCBI GI g2842496
 BLAST score 425
 E value 5.0e-42
 Match length 103
 % identity 80
 NCBI Description (AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 236618
 Seq. ID uC-gsflnu33B101b04b1
 Method BLASTX
 NCBI GI g2642445
 BLAST score 368
 E value 3.0e-35
 Match length 136

% identity 57
 NCBI Description (AC002391) putative serine/threonine protein kinase
 [Arabidopsis thaliana]

Seq. No. 236619
 Seq. ID uC-gsflnu33B101b07b1
 Method BLASTX
 NCBI GI g4512263
 BLAST score 520
 E value 4.0e-53
 Match length 128
 % identity 78
 NCBI Description (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]

Seq. No. 236620
 Seq. ID uC-gsflnu33B101c03b1
 Method BLASTX
 NCBI GI g1172995
 BLAST score 268
 E value 2.0e-23
 Match length 107
 % identity 52
 NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir_S52084 ribosomal
 protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
 ribosomal protein L22 [Rattus norvegicus]
 >gi_1093952_prf_2105193A ribosomal protein L22 [Rattus
 norvegicus]

Seq. No. 236621
 Seq. ID uC-gsflnu33B101d03b1
 Method BLASTX
 NCBI GI g544370
 BLAST score 203
 E value 7.0e-16
 Match length 55
 % identity 64
 NCBI Description GAR1 PROTEIN >gi_422064_pir_S33691 GAR1 protein - fission
 yeast (Schizosaccharomyces pombe) >gi_297009_emb_CAA79628_
 (Z19576) snoRNP protein GAR1 [Schizosaccharomyces pombe]
 >gi_1799516_dbj_BAA19143_ (AB000537) snoRNP protein GAR 1
 [Schizosaccharomyces pombe] >gi_2104450_emb_CAB08787_
 (Z95397) Garlp [Schizosaccharomyces pombe]
 >gi_2842463_emb_CAA16841.1_ (AL021747) gar1 protein; small
 nucleolar rnp required for pre-mrna for pre-mrna processing
 [Schizosaccharomyces pombe]

Seq. No. 236622
 Seq. ID uC-gsflnu33B101d11b1
 Method BLASTX
 NCBI GI g3096945
 BLAST score 400
 E value 5.0e-39
 Match length 110
 % identity 73
 NCBI Description (AL023094) putative auxin-regulated protein [Arabidopsis
 thaliana]

Seq. ID uC-gsflnu33B107a07b1
 Method BLASTX
 NCBI GI g2695711
 BLAST score 211
 E value 6.0e-17
 Match length 57
 % identity 63
 NCBI Description (AJ001370) cytochrome b5 [Olea europaea]

Seq. No. 236629
 Seq. ID uC-gsflnu33B107b10b1
 Method BLASTX
 NCBI GI g3426036
 BLAST score 242
 E value 2.0e-20
 Match length 144
 % identity 43
 NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 236630
 Seq. ID uC-gsflnu33B107b12b1
 Method BLASTX
 NCBI GI g1946372
 BLAST score 267
 E value 2.0e-23
 Match length 82
 % identity 65
 NCBI Description (U93215) yeast hypothetical protein YDB1_SCHPO isolog [Arabidopsis thaliana]

Seq. No. 236631
 Seq. ID uC-gsflnu33B107c08b1
 Method BLASTX
 NCBI GI g3785973
 BLAST score 171
 E value 5.0e-12
 Match length 49
 % identity 76
 NCBI Description (AC005560) putative homeobox protein [Arabidopsis thaliana]

Seq. No. 236632
 Seq. ID uC-gsflnu33B107c10b1
 Method BLASTX
 NCBI GI g4580523
 BLAST score 136
 E value 1.0e-08
 Match length 32
 % identity 84
 NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No. 236633
 Seq. ID uC-gsflnu33B107g07b1
 Method BLASTX
 NCBI GI g4388726
 BLAST score 148
 E value 2.0e-09
 Match length 40

09684016-101000

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Seq. No.      236641
Seq. ID       uC-gsflnu33B108d01b1
Method        BLASTX
NCBI GI       g1363484
BLAST score    341
E value        5.0e-32
Match length   103
% identity     66
NCBI Description IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415)
                IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin
                inducible protein, IAA13 [Arabidopsis thaliana]
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Seq. No.          236643
Seq. ID           uC-gsflnu33B108e08b1
Method            BLASTX
NCBI GI           g3334244
BLAST score       380
E value           1.0e-36
Match length      88
% identity        80
NCBI Description   LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
                  (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                  MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                  >gi_2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica
                  juncea]
```

34317

NCBI GI g2262118
 BLAST score 140
 E value 5.0e-09
 Match length 35
 % identity 80
 NCBI Description (AC002343) cell division protein isolog [Arabidopsis thaliana]

Seq. No. 236645
 Seq. ID uC-gsflnu33B108f04b1
 Method BLASTX
 NCBI GI g2505870
 BLAST score 156
 E value 3.0e-10
 Match length 48
 % identity 56
 NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236646
 Seq. ID uC-gsflnu33B108g11b1
 Method BLASTX
 NCBI GI g2827715
 BLAST score 468
 E value 5.0e-47
 Match length 129
 % identity 69
 NCBI Description (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 236647
 Seq. ID uC-gsflnu33B108h04b1
 Method BLASTX
 NCBI GI g2244835
 BLAST score 283
 E value 3.0e-25
 Match length 91
 % identity 62
 NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 236648
 Seq. ID uC-gsflnu33B109a02b1
 Method BLASTX
 NCBI GI g4006829
 BLAST score 459
 E value 9.0e-46
 Match length 168
 % identity 55
 NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 236649
 Seq. ID uC-gsflnu33B109b02b1
 Method BLASTX
 NCBI GI g3135274
 BLAST score 196
 E value 3.0e-15
 Match length 76
 % identity 53

NCBI Description (AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No. 236650
Seq. ID uC-gsflnu33B109d01b1
Method BLASTX
NCBI GI g3738283
BLAST score 402
E value 3.0e-39
Match length 82
% identity 85

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 236651
Seq. ID uC-gsflnu33B109d04b1
Method BLASTX
NCBI GI g3461817
BLAST score 178
E value 6.0e-13
Match length 64
% identity 56

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 236652
Seq. ID uC-gsflnu33B109e02b1
Method BLASTX
NCBI GI g3785999
BLAST score 349
E value 6.0e-33
Match length 91
% identity 73
NCBI Description (AC005499) putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]

Seq. No. 236653
Seq. ID uC-gsflnu33B109f02b1
Method BLASTX
NCBI GI g4006914
BLAST score 246
E value 8.0e-21
Match length 72
% identity 71
NCBI Description (Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]

Seq. No. 236654
Seq. ID uC-gsflnu33B109f03b1
Method BLASTX
NCBI GI g1173043
BLAST score 308
E value 4.0e-28
Match length 65
% identity 92
NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi_479441_pir_S33899.ribosomal protein L38 - tomato (cv. MoneyMaker)
>gi_313027_emb_CAA49599 (X69979) ribosomal protein L38 [Lycopersicon esculentum]

BLAST score 220
 E value 3.0e-18
 Match length 60
 % identity 73
 NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236666
 Seq. ID uC-gsflnu33B111d04b1
 Method BLASTX
 NCBI GI g4432821
 BLAST score 196
 E value 6.0e-15
 Match length 123
 % identity 39
 NCBI Description (AC006593) putative transmembrane protein [Arabidopsis thaliana]

Seq. No. 236667
 Seq. ID uC-gsflnu33B111d08b1
 Method BLASTX
 NCBI GI g113116
 BLAST score 573
 E value 4.0e-59
 Match length 175
 % identity 60
 NCBI Description ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
 >gi_111396_pir_A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase [Rattus norvegicus]

Seq. No. 236668
 Seq. ID uC-gsflnu33B111e08b1
 Method BLASTX
 NCBI GI g3236259
 BLAST score 736
 E value 3.0e-78
 Match length 163
 % identity 82
 NCBI Description (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 236669
 Seq. ID uC-gsflnu33B111e12b1
 Method BLASTX
 NCBI GI g4049347
 BLAST score 418
 E value 6.0e-41
 Match length 169
 % identity 50
 NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 236670
 Seq. ID uC-gsflnu33B111g03b1
 Method BLASTX
 NCBI GI g3024491
 BLAST score 206
 E value 4.0e-16

BLAST score 244
 E value 1.0e-20
 Match length 110
 % identity 52
 NCBI Description (AJ010463) RNA helicase [Arabidopsis thaliana]

Seq. No. 236708
 Seq. ID uC-gsflnu33B115e09b1
 Method BLASTX
 NCBI GI g4219092
 BLAST score 277
 E value 2.0e-24
 Match length 75
 % identity 72
 NCBI Description (AF117707) putative copper/zinc superoxide dismutase copper chaperone precursor [Lycopersicon esculentum]

Seq. No. 236709
 Seq. ID uC-gsflnu33B115e11b1
 Method BLASTX
 NCBI GI g1076291
 BLAST score 378
 E value 1.0e-36
 Match length 95
 % identity 75
 NCBI Description amino acid transporter AAT1 - Arabidopsis thaliana
 >gi_2911069_emb_CAA17531_ (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]

Seq. No. 236710
 Seq. ID uC-gsflnu33B115f02b1
 Method BLASTX
 NCBI GI g2832629
 BLAST score 182
 E value 2.0e-13
 Match length 87
 % identity 45
 NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No. 236711
 Seq. ID uC-gsflnu33B115f08b1
 Method BLASTX
 NCBI GI g3241945
 BLAST score 269
 E value 9.0e-24
 Match length 76
 % identity 57
 NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

Seq. No. 236712
 Seq. ID uC-gsflnu33B115g02b1
 Method BLASTX
 NCBI GI g3335378
 BLAST score 303
 E value 1.0e-27
 Match length 72

% identity	76
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]
Seq. No.	236713
Seq. ID	uC-gsflnu33B115g04b1
Method	BLASTX
NCBI GI	g2570338
BLAST score	213
E value	6.0e-17
Match length	69
% identity	61
NCBI Description	(U90927) glyoxalase II isozyme [Arabidopsis thaliana]
Seq. No.	236714
Seq. ID	uC-gsflnu33B115g05b1
Method	BLASTX
NCBI GI	g2245131
BLAST score	197
E value	3.0e-15
Match length	58
% identity	74
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.	236715
Seq. ID	uC-gsflnu33B115g07b1
Method	BLASTX
NCBI GI	g1495806
BLAST score	255
E value	6.0e-22
Match length	117
% identity	44
NCBI Description	(X95514) lipoxygenase [Solanum tuberosum]
Seq. No.	236716
Seq. ID	uC-gsflnu33B115h07b1
Method	BLASTX
NCBI GI	g4567248
BLAST score	199
E value	2.0e-16
Match length	95
% identity	49
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.	236717
Seq. ID	uC-gsflnu33B126a12b1
Method	BLASTX
NCBI GI	g2708745
BLAST score	438
E value	1.0e-43
Match length	96
% identity	49
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]
Seq. No.	236718
Seq. ID	uC-gsflnu33B126b01b1

Method BLASTX
 NCBI GI g4539314
 BLAST score 194
 E value 2.0e-15
 Match length 59
 % identity 64
 NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 236719
 Seq. ID uC-gsflnu33B126b08b1
 Method BLASTX
 NCBI GI g629602
 BLAST score 243
 E value 8.0e-31
 Match length 90
 % identity 76
 NCBI Description probable imbibition protein - wild cabbage
 >gi_488787_emb_CAA55893_(X79330) putative imbibition
 protein [Brassica oleracea]

Seq. No. 236720
 Seq. ID uC-gsflnu33B126f12b1
 Method BLASTX
 NCBI GI g2673914
 BLAST score 314
 E value 8.0e-29
 Match length 154
 % identity 49
 NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236721
 Seq. ID uC-gsflnu33B126g11b1
 Method BLASTX
 NCBI GI g1778376
 BLAST score 604
 E value 7.0e-63
 Match length 148
 % identity 78
 NCBI Description (U81288) PsRT17-1 [Pisum sativum]

Seq. No. 236722
 Seq. ID uC-gsflnu33B126h04b1
 Method BLASTX
 NCBI GI g3831467
 BLAST score 161
 E value 3.0e-11
 Match length 78
 % identity 40
 NCBI Description (AC005700) putative beta-amylase [Arabidopsis thaliana]

Seq. No. 236723
 Seq. ID uC-gsflnu33B126h10b1
 Method BLASTX
 NCBI GI g1769907
 BLAST score 142
 E value 1.0e-08
 Match length 32

protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
subunit ribosomal protein [Oryza sativa]

Seq. No. 236729
Seq. ID uC-gsflnu33B127c10b1
Method BLASTX
NCBI GI g3122572
BLAST score 739
E value 1.0e-78
Match length 143
% identity 97
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
SUBUNIT) >gi_1084434_pir_S52737 NADH dehydrogenase
(ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
>gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
complex I subunit [Solanum tuberosum]

Seq. No. 236730
Seq. ID uC-gsflnu33B127g02b1
Method BLASTX
NCBI GI g2213584
BLAST score 338
E value 8.0e-32
Match length 120
% identity 58
NCBI Description (AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No. 236731
Seq. ID uC-gsflnu33B127g11b1
Method BLASTX
NCBI GI g4539010
BLAST score 143
E value 7.0e-09
Match length 131
% identity 39
NCBI Description (AL049481) putative DNA-directed RNA polymerase
[Arabidopsis thaliana]

Seq. No. 236732
Seq. ID uC-gsflnu33B128b07b1
Method BLASTX
NCBI GI g2342676
BLAST score 568
E value 1.0e-58
Match length 129
% identity 81
NCBI Description (AC000106) Strong similarity to Oryza NADPH oxidase
(gb_X93301). [Arabidopsis thaliana]

Seq. No. 236733
Seq. ID uC-gsflnu33B128c04b1
Method BLASTX
NCBI GI g3395431
BLAST score 378
E value 2.0e-36
Match length 85

% identity 84
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

 Seq. No. 236734
 Seq. ID uC-gsflnu33B128c06b1
 Method BLASTX
 NCBI GI g3033375
 BLAST score 305
 E value 7.0e-28
 Match length 128
 % identity 48
 NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

 Seq. No. 236735
 Seq. ID uC-gsflnu33B128d02b1
 Method BLASTX
 NCBI GI g3834322
 BLAST score 268
 E value 1.0e-23
 Match length 87
 % identity 61
 NCBI Description (AC005679) EST gb_R30300 comes from this gene. [Arabidopsis thaliana]

 Seq. No. 236736
 Seq. ID uC-gsflnu33B128d11b1
 Method BLASTX
 NCBI GI g2832304
 BLAST score 347
 E value 6.0e-33
 Match length 115
 % identity 60
 NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]

 Seq. No. 236737
 Seq. ID uC-gsflnu33B128e11b1
 Method BLASTX
 NCBI GI g2129921
 BLAST score 178
 E value 4.0e-13
 Match length 35
 % identity 94
 NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi_758694 (U12573) putative [Catharanthus roseus]

 Seq. No. 236738
 Seq. ID uC-gsflnu33B128f02b1
 Method BLASTX
 NCBI GI g4098246
 BLAST score 356
 E value 6.0e-34
 Match length 116
 % identity 63
 NCBI Description (U76410) homeobox 2 protein [Lycopersicon esculentum]

 Seq. No. 236739

Seq. ID uC-gsflnu33B128f10b1
 Method BLASTX
 NCBI GI g3236241
 BLAST score 371
 E value 1.0e-35
 Match length 100
 % identity 66
 NCBI Description (AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 236740
 Seq. ID uC-gsflnu33B128g10b1
 Method BLASTX
 NCBI GI g1168470
 BLAST score 239
 E value 4.0e-20
 Match length 109
 % identity 54
 NCBI Description PROTEIN KINASE APK1A >gi_282877_pir_S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No. 236741
 Seq. ID uC-gsflnu33B129d05b1
 Method BLASTX
 NCBI GI g4115383
 BLAST score 284
 E value 2.0e-25
 Match length 119
 % identity 18
 NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 236742
 Seq. ID uC-gsflnu33B129e01b1
 Method BLASTX
 NCBI GI g2062172
 BLAST score 379
 E value 9.0e-37
 Match length 82
 % identity 83
 NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]

Seq. No. 236743
 Seq. ID uC-gsflnu33B129e04b1
 Method BLASTX
 NCBI GI g2935298
 BLAST score 472
 E value 2.0e-47
 Match length 97
 % identity 97
 NCBI Description (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

Seq. No. 236744

Seq. ID uC-gsflnu33B130a03b1
 Method BLASTX
 NCBI GI g3746060
 BLAST score 235
 E value 1.0e-19
 Match length 59
 % identity 68
 NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 236745
 Seq. ID uC-gsflnu33B130a07b1
 Method BLASTX
 NCBI GI g2920706
 BLAST score 231
 E value 4.0e-19
 Match length 97
 % identity 46
 NCBI Description (Y13568) beta-xylosidase [Emericella nidulans]

Seq. No. 236746
 Seq. ID uC-gsflnu33B130b04b1
 Method BLASTX
 NCBI GI g231660
 BLAST score 341
 E value 4.0e-32
 Match length 131
 % identity 62
 NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No. 236747
 Seq. ID uC-gsflnu33B130d08b1
 Method BLASTX
 NCBI GI g125393
 BLAST score 176
 E value 7.0e-13
 Match length 101
 % identity 39
 NCBI Description HOMOSERINE KINASE (HK) >gi_79795_pir_S03743 homoserine kinase (EC 2.7.1.39) - Calothrix sp. >gi_43396_emb_CAA68576_ (Y00522) homoserine kinase (AA 1-307) [Calothrix PCC7601]

Seq. No. 236748
 Seq. ID uC-gsflnu33B130f05b1
 Method BLASTX
 NCBI GI g1705930
 BLAST score 312
 E value 1.0e-28
 Match length 93
 % identity 68
 NCBI Description ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1 (ENDOPEPTIDASE CLP 1) >gi_1001349_dbj_BAA10836_ (D64006) ATP-dependent protease ClpP [Synechocystis sp.]

Seq. No. 236749
 Seq. ID uC-gsflnu33B130h09b1
 Method BLASTX
 NCBI GI g4234955

BLAST score 217
 E value 2.0e-17
 Match length 109
 % identity 25
 NCBI Description (AF098971) NBS-LRR-like protein CD8 [Phaseolus vulgaris]

Seq. No. 236750
 Seq. ID uC-gsflnu33B131a01b1
 Method BLASTX
 NCBI GI g3273243
 BLAST score 537
 E value 3.0e-55
 Match length 120
 % identity 29
 NCBI Description (AB004660) NLS receptor [Oryza sativa]
 >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza sativa]

Seq. No. 236751
 Seq. ID uC-gsflnu33B131a04b1
 Method BLASTX
 NCBI GI g1518113
 BLAST score 155
 E value 7.0e-11
 Match length 52
 % identity 54
 NCBI Description (U66193) SLL2 [Brassica napus]

Seq. No. 236752
 Seq. ID uC-gsflnu33B131c01b1
 Method BLASTX
 NCBI GI g2462760
 BLAST score 287
 E value 8.0e-26
 Match length 119
 % identity 51
 NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 236753
 Seq. ID uC-gsflnu33B131e01b1
 Method BLASTX
 NCBI GI g4539351
 BLAST score 255
 E value 4.0e-22
 Match length 116
 % identity 44
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 236754
 Seq. ID uC-gsflnu33B131e12b1
 Method BLASTX
 NCBI GI g2865623
 BLAST score 282
 E value 2.0e-25
 Match length 67
 % identity 79
 NCBI Description (AF045286)

GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
[Arabidopsis thaliana]

Seq. No.	236755
Seq. ID	uC-gsflnu33B131f03b1
Method	BLASTX
NCBI GI	g3005931
BLAST score	398
E value	9.0e-39
Match length	129
% identity	42
NCBI Description	(AJ005016) ABC transporter [Homo sapiens]
Seq. No.	236756
Seq. ID	uC-gsflnu33B131f10b1
Method	BLASTX
NCBI GI	g3046995
BLAST score	178
E value	3.0e-13
Match length	86
% identity	44
NCBI Description	(AF056717) ash212 [Homo sapiens]
Seq. No.	236757
Seq. ID	uC-gsflnu33B131h02b1
Method	BLASTX
NCBI GI	g1621463
BLAST score	250
E value	9.0e-22
Match length	49
% identity	88
NCBI Description	(U73104) laccase [Liriodendron tulipifera]
Seq. No.	236758
Seq. ID	uC-gsflnu33B131h10b1
Method	BLASTX
NCBI GI	g2462748
BLAST score	137
E value	9.0e-09
Match length	27
% identity	100
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]
Seq. No.	236759
Seq. ID	uC-gsflnu33B132e12b1
Method	BLASTX
NCBI GI	g139799
BLAST score	266
E value	2.0e-23
Match length	102
% identity	53
NCBI Description	XANTHINE DEHYDROGENASE (XD) (ROSY LOCUS PROTEIN) >gi_8831_emb_CAA68409_ (Y00308) xanthine dehydrogenase [Drosophila melanogaster]
Seq. No.	236760

Seq. ID uC-gsflnu33B132g01b1
 Method BLASTX
 NCBI GI g2673912
 BLAST score 167
 E value 9.0e-12
 Match length 46
 % identity 74
 NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]

Seq. No. 236761
 Seq. ID uC-gsflnu33B132h10b1
 Method BLASTX
 NCBI GI g4454051
 BLAST score 572
 E value 4.0e-59
 Match length 139
 % identity 76
 NCBI Description (AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 236762
 Seq. ID uC-gsflnu33B132h12b1
 Method BLASTX
 NCBI GI g4544427
 BLAST score 286
 E value 2.0e-25
 Match length 76
 % identity 82
 NCBI Description (AC006955) putative ferredoxin-thioredoxin reductase [Arabidopsis thaliana]

Seq. No. 236763
 Seq. ID uC-gsflnu33B133b03b1
 Method BLASTX
 NCBI GI g2827715
 BLAST score 280
 E value 2.0e-25
 Match length 71
 % identity 77
 NCBI Description (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 236764
 Seq. ID uC-gsflnu33B133b07b1
 Method BLASTX
 NCBI GI g1498338
 BLAST score 366
 E value 3.0e-35
 Match length 79
 % identity 95
 NCBI Description (U60502) actin [Glycine max]

Seq. No. 236765
 Seq. ID uC-gsflnu33B133f12b1
 Method BLASTX
 NCBI GI g129590
 BLAST score 567

E value 9.0e-59
 Match length 116
 % identity 94
 NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_99990_pir_S17444
 phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - alfalfa
 >gi_19650_emb_CAA41169_ (X58180) phenylalanine
 ammonia-lyase [Medicago sativa]

Seq. No. 236766
 Seq. ID uC-gsflnu33B133h09b1
 Method BLASTX
 NCBI GI g422029
 BLAST score 292
 E value 2.0e-26
 Match length 66
 % identity 77
 NCBI Description transcription factor OBF3.2, ocs element-binding - maize
 >gi_297018_emb_CAA48904_ (X69152) ocs-element binding
 factor 3.2 [Zea mays]

Seq. No. 236767
 Seq. ID uC-gsflnu33B134b08b1
 Method BLASTX
 NCBI GI g3242789
 BLAST score 515
 E value 2.0e-52
 Match length 136
 % identity 76
 NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis
 thaliana]

Seq. No. 236768
 Seq. ID uC-gsflnu33B134b12b1
 Method BLASTX
 NCBI GI g2244835
 BLAST score 261
 E value 7.0e-23
 Match length 80
 % identity 64
 NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 236769
 Seq. ID uC-gsflnu33B134c10b1
 Method BLASTX
 NCBI GI g4388727
 BLAST score 226
 E value 9.0e-19
 Match length 76
 % identity 61
 NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236770
 Seq. ID uC-gsflnu33B135a10b1
 Method BLASTX
 NCBI GI g1174592
 BLAST score 343
 E value 8.0e-53

NCBI GI g2288988
 BLAST score 231
 E value 3.0e-19
 Match length 113
 % identity 41
 NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236776
 Seq. ID uC-gsflnu33B136c12b1
 Method BLASTX
 NCBI GI g4490303
 BLAST score 410
 E value 4.0e-40
 Match length 99
 % identity 77
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 236777
 Seq. ID uC-gsflnu33B136d07b1
 Method BLASTX
 NCBI GI g3763933
 BLAST score 192
 E value 4.0e-15
 Match length 67
 % identity 76
 NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 236778
 Seq. ID uC-gsflnu33B136e02b1
 Method BLASTX
 NCBI GI g135392
 BLAST score 153
 E value 3.0e-10
 Match length 46
 % identity 63
 NCBI Description TUBULIN ALPHA-1 CHAIN >gi_101808_pir_S13336 tubulin
 alpha-1 chain - Emericella nidulans

Seq. No. 236779
 Seq. ID uC-gsflnu33B136e04b1
 Method BLASTX
 NCBI GI g2982268
 BLAST score 280
 E value 4.0e-25
 Match length 57
 % identity 93
 NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea
 mariana]

Seq. No. 236780
 Seq. ID uC-gsflnu33B136g01b1
 Method BLASTX
 NCBI GI g3980377
 BLAST score 416
 E value 7.0e-41
 Match length 140
 % identity 61

Method BLASTX
 NCBI GI g1174595
 BLAST score 416
 E value 6.0e-41
 Match length 105
 % identity 56
 NCBI Description TUBULIN BETA-1 CHAIN >gi_1076658_pir_S50747 beta-tubulin -
 potato >gi_609268_emb_CAA83847_ (Z33382) beta-tubulin
 [Solanum tuberosum]

Seq. No. 236787
 Seq. ID uC-gsflnu33B137f01b1
 Method BLASTX
 NCBI GI g3915737
 BLAST score 255
 E value 4.0e-22
 Match length 57
 % identity 89
 NCBI Description IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP
 ALPHA) >gi_3228370 (AF017252) importin alpha [Lycopersicon
 esculentum]

Seq. No. 236788
 Seq. ID uC-gsflnu33B137g12b1
 Method BLASTX
 NCBI GI g3451074
 BLAST score 592
 E value 2.0e-61
 Match length 135
 % identity 76
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 236789
 Seq. ID uC-gsflnu33B137h11b1
 Method BLASTX
 NCBI GI g2252841
 BLAST score 176
 E value 2.0e-16
 Match length 81
 % identity 57
 NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 236790
 Seq. ID uC-gsflnu33B138a09b1
 Method BLASTX
 NCBI GI g1495366
 BLAST score 234
 E value 1.0e-19
 Match length 134
 % identity 41
 NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 236791
 Seq. ID uC-gsflnu33B138b07b1
 Method BLASTX
 NCBI GI g4455364
 BLAST score 174

E value 1.0e-12
 Match length 42
 % identity 79
 NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No. 236792
 Seq. ID uC-gsflnu33B138b10b1
 Method BLASTX
 NCBI GI g2827528
 BLAST score 473
 E value 2.0e-47
 Match length 132
 % identity 69
 NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 236793
 Seq. ID uC-gsflnu33B138c10b1
 Method BLASTX
 NCBI GI g1871192
 BLAST score 612
 E value 8.0e-64
 Match length 127
 % identity 81
 NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 236794
 Seq. ID uC-gsflnu33B138c12b1
 Method BLASTX
 NCBI GI g1279600
 BLAST score 433
 E value 5.0e-43
 Match length 104
 % identity 77
 NCBI Description (Z71753) pectin methylesterase [Nicotiana plumbaginifolia]

Seq. No. 236795
 Seq. ID uC-gsflnu33B138d11b1
 Method BLASTX
 NCBI GI g4510368
 BLAST score 331
 E value 2.0e-31
 Match length 138
 % identity 61
 NCBI Description (AC007017) putative transcription factor E2F5 [Arabidopsis thaliana]

Seq. No. 236796
 Seq. ID uC-gsflnu33B138f12b1
 Method BLASTX
 NCBI GI g3860256
 BLAST score 177
 E value 7.0e-13
 Match length 70
 % identity 54
 NCBI Description (AC005824) putative tRNA isopentenylpyrophosphate

thaliana]

Seq. No. 236802
 Seq. ID uC-gsflnu33B140a09b1
 Method BLASTX
 NCBI GI g464981
 BLAST score 683
 E value 4.0e-72
 Match length 142
 % identity 87
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 236803
 Seq. ID uC-gsflnu33B140b01b1
 Method BLASTX
 NCBI GI g2443886
 BLAST score 383
 E value 4.0e-37
 Match length 91
 % identity 81
 NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 236804
 Seq. ID uC-gsflnu33B140b06b1
 Method BLASTX
 NCBI GI g3510254
 BLAST score 494
 E value 5.0e-50
 Match length 108
 % identity 88
 NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 236805
 Seq. ID uC-gsflnu33B140c01b1
 Method BLASTX
 NCBI GI g1771780
 BLAST score 430
 E value 2.0e-42
 Match length 106
 % identity 78
 NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 236806
 Seq. ID uC-gsflnu33B140d06b1
 Method BLASTX
 NCBI GI g3236241
 BLAST score 365
 E value 7.0e-35
 Match length 103
 % identity 71
 NCBI Description (AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 236807
 Seq. ID uC-gsflnu33B140d10b1

E value 1.0e-19
 Match length 133
 % identity 36
 NCBI Description (AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No. 236813
 Seq. ID uC-gsflnu33B141d09b1
 Method BLASTX
 NCBI GI g1709692
 BLAST score 461
 E value 3.0e-46
 Match length 101
 % identity 84
 NCBI Description PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O) REDUCTASE) (FRUIT-RIPENING PROTEIN E4)
 >gi_100204_pir_JQ0988 DNA-binding E4 protein - Tomato

Seq. No. 236814
 Seq. ID uC-gsflnu33B141d12b1
 Method BLASTX
 NCBI GI g2921323
 BLAST score 383
 E value 7.0e-37
 Match length 139
 % identity 56
 NCBI Description (AF034112) beta-1,3-glucanase 7 [Glycine max]

Seq. No. 236815
 Seq. ID uC-gsflnu33B141h04b1
 Method BLASTX
 NCBI GI g3169719
 BLAST score 255
 E value 2.0e-22
 Match length 80
 % identity 66
 NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]

Seq. No. 236816
 Seq. ID uC-gsflnu33B142b04b1
 Method BLASTX
 NCBI GI g2632105
 BLAST score 144
 E value 5.0e-09
 Match length 55
 % identity 58
 NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
 >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 236817
 Seq. ID uC-gsflnu33B142g02b1
 Method BLASTX
 NCBI GI g2702279
 BLAST score 283
 E value 7.0e-26
 Match length 69

% identity	78
NCBI Description	(AC003033) putative phosphate transporter [Arabidopsis thaliana] >gi_2780345_dbj_BAA24280_ (AB000093) inorganic phosphate transporter [Arabidopsis thaliana] >gi_2914691 (AC003974) putative phosphate transporter [Arabidopsis thaliana]
Seq. No.	236818
Seq. ID	uC-gsflnu33B142g04b1
Method	BLASTX
NCBI GI	g4263519
BLAST score	435
E value	3.0e-43
Match length	89
% identity	93
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]
Seq. No.	236819
Seq. ID	uC-gsflnu33B143a06b1
Method	BLASTX
NCBI GI	g584892
BLAST score	354
E value	1.0e-33
Match length	123
% identity	56
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) >gi_629805_pir_S43516 serine carboxypeptidase I - rice >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I [Oryza sativa]
Seq. No.	236820
Seq. ID	uC-gsflnu33B143a07b1
Method	BLASTX
NCBI GI	g3287693
BLAST score	617
E value	2.0e-64
Match length	150
% identity	73
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]
Seq. No.	236821
Seq. ID	uC-gsflnu33B143b09b1
Method	BLASTX
NCBI GI	g4567228
BLAST score	268
E value	1.0e-23
Match length	74
% identity	65
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]
Seq. No.	236822
Seq. ID	uC-gsflnu33B143d03b1
Method	BLASTX
NCBI GI	g1653395

BLAST score 362
 E value 2.0e-34
 Match length 141
 % identity 50
 NCBI Description (D90913) PET112 [Synechocystis sp.]

Seq. No. 236823
 Seq. ID uC-gsflnu33B143e09b1
 Method BLASTX
 NCBI GI g1706263
 BLAST score 322
 E value 7.0e-30
 Match length 129
 % identity 48
 NCBI Description CYSTEINE PROTEINASE 5 PRECURSOR >gi_1222694 (L36205) CP5 [Dictyostelium discoideum]

Seq. No. 236824
 Seq. ID uC-gsflnu33B143f02b1
 Method BLASTX
 NCBI GI g1076809
 BLAST score 459
 E value 5.0e-46
 Match length 125
 % identity 78
 NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase [Zea mays]

Seq. No. 236825
 Seq. ID uC-gsflnu33B143f06b1
 Method BLASTX
 NCBI GI g4426964
 BLAST score 331
 E value 6.0e-31
 Match length 80
 % identity 71
 NCBI Description (AF126255) purple acid phosphatase precursor [Anchusa officinalis]

Seq. No. 236826
 Seq. ID uC-gsflnu33B143g12b1
 Method BLASTX
 NCBI GI g4249384
 BLAST score 241
 E value 3.0e-20
 Match length 99
 % identity 44
 NCBI Description (AC005966) Similar to gi_4056506 F3G5.25 nodulin-like protein from Arabidopsis thaliana BAC gb_AC005896. [Arabidopsis thaliana]

Seq. No. 236827
 Seq. ID uC-gsflnu33B143h10b1
 Method BLASTX
 NCBI GI g1172977
 BLAST score 562

NCBI Description immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406
(U52046) immunophilin [Arabidopsis thaliana]

Seq. No. 236843
Seq. ID uC-gsflnu33B145c05b1
Method BLASTX
NCBI GI g3643603
BLAST score 460
E value 4.0e-46
Match length 126
% identity 73
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 236844
Seq. ID uC-gsflnu33B145d02b1
Method BLASTX
NCBI GI g2723477
BLAST score 617
E value 2.0e-64
Match length 149
% identity 80
NCBI Description (D89824) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 236845
Seq. ID uC-gsflnu33B145e04b1
Method BLASTX
NCBI GI g4455202
BLAST score 458
E value 1.0e-45
Match length 146
% identity 60
NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 236846
Seq. ID uC-gsflnu33B145e06b1
Method BLASTX
NCBI GI g1172597
BLAST score 226
E value 1.0e-18
Match length 47
% identity 91
NCBI Description WOUND-INDUCED BASIC PROTEIN >gi_81888_pir_JS0731
wound-inducible basic protein - kidney bean >gi_169365
(L00625) basic protein [Phaseolus vulgaris]
>gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein
[Phaseolus vulgaris]

Seq. No. 236847
Seq. ID uC-gsflnu33B145e10b1
Method BLASTX
NCBI GI g2662415
BLAST score 173
E value 2.0e-12
Match length 56
% identity 54
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No. 236848
 Seq. ID uC-gsflnu33B145f01b1
 Method BLASTX
 NCBI GI g3980384
 BLAST score 351
 E value 3.0e-33
 Match length 109
 % identity 61
 NCBI Description (AC004561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236849
 Seq. ID uC-gsflnu33B145f06b1
 Method BLASTX
 NCBI GI g21309
 BLAST score 341
 E value 4.0e-32
 Match length 81
 % identity 42
 NCBI Description (X57955) 28kD RNA binding protein [Spinacia oleracea]

Seq. No. 236850
 Seq. ID uC-gsflnu33B145g05b1
 Method BLASTX
 NCBI GI g3152560
 BLAST score 176
 E value 8.0e-13
 Match length 65
 % identity 51
 NCBI Description (AC002986) Strong similarity to ser/thr protein kinases, especially gb_X97980 from solanum berthaultii, gb_X90990 from solanum tuberosum and gb_D10909 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 236851
 Seq. ID uC-gsflnu33B145g06b1
 Method BLASTX
 NCBI GI g21309
 BLAST score 346
 E value 1.0e-32
 Match length 79
 % identity 43
 NCBI Description (X57955) 28kD RNA binding protein [Spinacia oleracea]

Seq. No. 236852
 Seq. ID uC-gsflnu33B145h10b1
 Method BLASTX
 NCBI GI g1223579
 BLAST score 215
 E value 2.0e-17
 Match length 108
 % identity 52
 NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

Seq. No. 236853
 Seq. ID uC-gsflnu33B146a01b1
 Method BLASTX
 NCBI GI g4559327

Method BLASTX
 NCBI GI g2288999
 BLAST score 153
 E value 5.0e-10
 Match length 127
 % identity 46
 NCBI Description (AC002335) electron transfer flavoprotein ubiquinone
 oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 236859
 Seq. ID uC-gsflnu33B146f12b1
 Method BLASTX
 NCBI GI g3641647
 BLAST score 447
 E value 1.0e-44
 Match length 101
 % identity 78
 NCBI Description (AB006804) ACC synthase [Cucumis sativus]

Seq. No. 236860
 Seq. ID uC-gsflnu33B146g01b1
 Method BLASTX
 NCBI GI g4240253
 BLAST score 141
 E value 6.0e-09
 Match length 75
 % identity 41
 NCBI Description (AB020689) KIAA0882 protein [Homo sapiens]

Seq. No. 236861
 Seq. ID uC-gsflnu33B146g04b1
 Method BLASTX
 NCBI GI g4115913
 BLAST score 508
 E value 1.0e-51
 Match length 152
 % identity 61
 NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of
 oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88,
 N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_
 (AL049524) putative flavanone 3-beta-hydroxylase
 [Arabidopsis thaliana]

Seq. No. 236862
 Seq. ID uC-gsronu33B001a07b1
 Method BLASTX
 NCBI GI g4106696
 BLAST score 262
 E value 9.0e-23
 Match length 68
 % identity 72
 NCBI Description (AB021872) ribosome-sedimenting protein [Pisum sativum]

Seq. No. 236863
 Seq. ID uC-gsronu33B001a09b1
 Method BLASTX
 NCBI GI g1850546

BLAST score 241
 E value 3.0e-20
 Match length 61
 % identity 74
 NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No. 236864
 Seq. ID uC-gsronu33B001c02b1
 Method BLASTX
 NCBI GI g4220469
 BLAST score 145
 E value 5.0e-09
 Match length 51
 % identity 63
 NCBI Description (AC006069) putative receptor protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No. 236865
 Seq. ID uC-gsronu33B001c04b1
 Method BLASTX
 NCBI GI g136057
 BLAST score 510
 E value 7.0e-52
 Match length 130
 % identity 75
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_99499_pir_A32187 (S)-tetrahydroberberine oxidase -
 Coptis japonica >gi_556171 (J04121) triosephosphate
 isomerase [Coptis japonica]

Seq. No. 236866
 Seq. ID uC-gsronu33B001c10b1
 Method BLASTX
 NCBI GI g1907076
 BLAST score 378
 E value 2.0e-36
 Match length 118
 % identity 60
 NCBI Description (Y07867) pirin [Homo sapiens] >gi_1907078_emb_CAA69195_
 (Y07868) pirin [Homo sapiens]
 >gi_4505823_ref_NP_003653.1_pPIR_pirin

Seq. No. 236867
 Seq. ID uC-gsronu33B001f03b1
 Method BLASTX
 NCBI GI g2979549
 BLAST score 376
 E value 4.0e-36
 Match length 128
 % identity 52
 NCBI Description (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No. 236868
 Seq. ID uC-gsronu33B001g03b1
 Method BLASTX

NCBI Description (AB010991) 3b-hydroxylase [*Lycopersicon esculentum*]

Seq. No. 236879
 Seq. ID uC-gsronu33B002h05b1
 Method BLASTX
 NCBI GI g2244855
 BLAST score 198
 E value 2.0e-15
 Match length 97
 % identity 45
 NCBI Description (Z97337) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 236880
 Seq. ID uC-gsronu33B004a01b1
 Method BLASTX
 NCBI GI g2262111
 BLAST score 234
 E value 5.0e-24
 Match length 81
 % identity 65
 NCBI Description (AC002343) ribitol dehydrogenase isolog [*Arabidopsis thaliana*]

Seq. No. 236881
 Seq. ID uC-gsronu33B004a06b1
 Method BLASTX
 NCBI GI g3377850
 BLAST score 147
 E value 8.0e-10
 Match length 39
 % identity 77
 NCBI Description (AF076274) contains similarity to *Canis familiaris* signal peptidase complex 25 kDa subunit (GB:U12687) [*Arabidopsis thaliana*]

Seq. No. 236882
 Seq. ID uC-gsronu33B004a08b1
 Method BLASTX
 NCBI GI g4522005
 BLAST score 167
 E value 1.0e-11
 Match length 86
 % identity 41
 NCBI Description (AC007069) putative reverse transcriptase [*Arabidopsis thaliana*]

Seq. No. 236883
 Seq. ID uC-gsronu33B004b02b1
 Method BLASTX
 NCBI GI g3242710
 BLAST score 282
 E value 2.0e-25
 Match length 102
 % identity 62
 NCBI Description (AC003040) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 236884

09684016-1010000

% identity 77
NCBI Description (AC004393) Similar to ERECTA receptor protein kinase
gb_U47029 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 236903
Seq. ID uC-gsronu33B008e02b1
Method BLASTX
NCBI GI g3603473
BLAST score 206
E value 4.0e-16
Match length 76
% identity 57

NCBI Description (AF090698) elicitor-responsive gene-3 [Oryza sativa]

Seq. No. 236904
Seq. ID uC-gsronu33B008e04b1
Method BLASTX
NCBI GI g4038352
BLAST score 239
E value 3.0e-20
Match length 101
% identity 47

NCBI Description (AF098951) breast cancer resistance protein [Homo sapiens]

Seq. No. 236905
Seq. ID uC-gsronu33B008f03b1
Method BLASTX
NCBI GI g2739360
BLAST score 433
E value 9.0e-43
Match length 145
% identity 63

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
>gi_3075385 (AC004484) unknown protein [Arabidopsis
thaliana]

Seq. No. 236906
Seq. ID uC-gsronu33B008f10b1
Method BLASTX
NCBI GI g2662415
BLAST score 173
E value 2.0e-12
Match length 56
% identity 54

NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]

Seq. No. 236907
Seq. ID uC-gsronu33B008f11b1
Method BLASTX
NCBI GI g4455190
BLAST score 473
E value 2.0e-47
Match length 121
% identity 78

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 236908

Seq. ID uC-gsronu33B008h12b1
 Method BLASTX
 NCBI GI g730463
 BLAST score 321
 E value 1.0e-29
 Match length 102
 % identity 60
 NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
 >gi_630323_pir_S44069 ribosomal protein L35a.e.c15 - yeast
 (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
 protein L37 [Saccharomyces cerevisiae]
 >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
 [Saccharomyces cerevisiae]

Seq. No. 236909
 Seq. ID uC-gsronu33B009a06b1
 Method BLASTX
 NCBI GI g2462781
 BLAST score 408
 E value 3.0e-40
 Match length 95
 % identity 75
 NCBI Description (U73175) carbamoyl phosphate synthetase small subunit
 [Arabidopsis thaliana]

Seq. No. 236910
 Seq. ID uC-gsronu33B011a09b1
 Method BLASTX
 NCBI GI g2829926
 BLAST score 186
 E value 6.0e-14
 Match length 116
 % identity 42
 NCBI Description (AC002291) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 236911
 Seq. ID uC-gsronu33B011c03b1
 Method BLASTX
 NCBI GI g1657948
 BLAST score 378
 E value 2.0e-36
 Match length 138
 % identity 89
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 236912
 Seq. ID uC-gsronu33B011d06b1
 Method BLASTX
 NCBI GI g2642432
 BLAST score 99
 E value 6.0e-09
 Match length 105
 % identity 47
 NCBI Description (AC002391) putative elicitor response element binding
 protein (WRKY3) [Arabidopsis thaliana]

Seq. No. 236913

BLAST score 193
 E value 9.0e-15
 Match length 79
 % identity 53
 NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 236924
 Seq. ID uC-gsronu33B012c05b1
 Method BLASTX
 NCBI GI g2213621
 BLAST score 196
 E value 5.0e-15
 Match length 50
 % identity 72
 NCBI Description (AC000103) F21J9.26 [Arabidopsis thaliana]

Seq. No. 236925
 Seq. ID uC-gsronu33B012c07b1
 Method BLASTX
 NCBI GI g3928150
 BLAST score 441
 E value 1.0e-43
 Match length 98
 % identity 90
 NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 236926
 Seq. ID uC-gsronu33B012c12b1
 Method BLASTX
 NCBI GI g3122673
 BLAST score 263
 E value 3.0e-24
 Match length 111
 % identity 57
 NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 236927
 Seq. ID uC-gsronu33B012d03b1
 Method BLASTX
 NCBI GI g984756
 BLAST score 147
 E value 3.0e-09
 Match length 90
 % identity 47
 NCBI Description (Z54153) chilling-inducible protein [Oryza sativa]

Seq. No. 236928
 Seq. ID uC-gsronu33B012e02b1
 Method BLASTX
 NCBI GI g1350707
 BLAST score 212
 E value 5.0e-17
 Match length 52
 % identity 73
 NCBI Description 60S RIBOSOMAL PROTEIN L29 >gi_539923_pir_JC2012 ribosomal protein 17K - mouse >gi_404766 (L08651) ribosomal protein

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Seq. No.          236930
Seq. ID           uC-gsronu33B012g10b1
Method            BLASTX
NCBI GI           g123379
BLAST score       141
E value           1.0e-08
Match length      31
% identity        84
NCBI Description  HMGl/2-LIKE PROTEIN (SB11 PROTEIN) >gi_99914_pir_S22309
                  HMG-1-like protein - soybean >gi_18645_emb_CAA41200-
                  (X58245) HMG-1 like protein gene [Glycine max]
```

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Seq. No.      236932
Seq. ID       uC-gsronu33B014e04b1
Method        BLASTX
NCBI GI       g1616614
BLAST score    207
E value        1.0e-16
Match length   40
% identity     100
NCBI Description (Y08425) small GTP-binding protein [Nicotiana
plumbaginifolia]
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>gi_83176_pir_S19389 hypothetical protein YCL059c - yeast
(Saccharomyces cerevisiae) >gi_5300_emb_CAA42386_ (X59720)
YCL059c, len:316 [Saccharomyces cerevisiae]

Seq. No. 236934
Seq. ID uC-gsronu33B014e12b1
Method BLASTX
NCBI GI g4220472
BLAST score 225
E value 4.0e-19
Match length 64
% identity 73
NCBI Description (AC006069) similar to yeast cccl protein [Arabidopsis thaliana]

Seq. No. 236935
Seq. ID uC-gsronu33B014g11b1
Method BLASTX
NCBI GI g2821957
BLAST score 141
E value 3.0e-09
Match length 56
% identity 50
NCBI Description (AB006691) spermidine synthase 2 [Hyoscyamus niger]

Seq. No. 236936
Seq. ID uC-gsronu33B015a06b1
Method BLASTX
NCBI GI g3548815
BLAST score 188
E value 4.0e-14
Match length 124
% identity 43
NCBI Description (AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]

Seq. No. 236937
Seq. ID uC-gsronu33B015a07b1
Method BLASTX
NCBI GI g3924601
BLAST score 463
E value 3.0e-46
Match length 116
% identity 80
NCBI Description (AF069442) putative rac GTPase activating protein [Arabidopsis thaliana] >gi_4262138_gb_AAD14438_ (AC005275) putative rac GTPase-activating protein [Arabidopsis thaliana]

Seq. No. 236938
Seq. ID uC-gsronu33B015b06b1
Method BLASTX
NCBI GI g2465923
BLAST score 388
E value 5.0e-43
Match length 144
% identity 62

BLAST score 588
 E value 5.0e-61
 Match length 135
 % identity 79
 NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 236961
 Seq. ID uC-gsronu33B017e10b1
 Method BLASTX
 NCBI GI g2281090
 BLAST score 317
 E value 2.0e-29
 Match length 98
 % identity 62
 NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236962
 Seq. ID uC-gsronu33B017g08b1
 Method BLASTX
 NCBI GI g2501056
 BLAST score 328
 E value 4.0e-31
 Match length 71
 % identity 85
 NCBI Description SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
 >gi_2129737_pir_S71293 seryl-tRNA synthetase - Arabidopsis
 thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA
 Synthetase [Arabidopsis thaliana]

Seq. No. 236963
 Seq. ID uC-gsronu33B018b01b1
 Method BLASTX
 NCBI GI g3063396
 BLAST score 384
 E value 8.0e-54
 Match length 118
 % identity 89
 NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 236964
 Seq. ID uC-gsronu33B018c01b1
 Method BLASTX
 NCBI GI g2738949
 BLAST score 453
 E value 3.0e-45
 Match length 93
 % identity 91
 NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x
 ananassa]

Seq. No. 236965
 Seq. ID uC-gsronu33B018c12b1
 Method BLASTX
 NCBI GI g4510376
 BLAST score 296
 E value 5.0e-27
 Match length 87

% identity	60
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.	236966
Seq. ID	uC-gsronu33B018d03b1
Method	BLASTX
NCBI GI	g4572674
BLAST score	274
E value	3.0e-24
Match length	61
% identity	79
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.	236967
Seq. ID	uC-gsronu33B018d07b1
Method	BLASTX
NCBI GI	g2827623
BLAST score	213
E value	4.0e-17
Match length	46
% identity	91
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]
Seq. No.	236968
Seq. ID	uC-gsronu33B018d11b1
Method	BLASTX
NCBI GI	g1657619
BLAST score	404
E value	2.0e-39
Match length	164
% identity	46
NCBI Description	(U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]
Seq. No.	236969
Seq. ID	uC-gsronu33B018f01b1
Method	BLASTX
NCBI GI	g3608412
BLAST score	334
E value	4.0e-31
Match length	99
% identity	65
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]
Seq. No.	236970
Seq. ID	uC-gsronu33B018f10b1
Method	BLASTX
NCBI GI	g3769671
BLAST score	350
E value	4.0e-33
Match length	81
% identity	78
NCBI Description	(AF095284) Tic22 [Pisum sativum]
Seq. No.	236971
Seq. ID	uC-gsronu33B018f12b1

Method BLASTX
 NCBI GI g2738949
 BLAST score 377
 E value 2.0e-36
 Match length 84
 % identity 85
 NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No. 236972
 Seq. ID uC-gsronu33B019a03b1
 Method BLASTX
 NCBI GI g1710551
 BLAST score 281
 E value 5.0e-25
 Match length 51
 % identity 100
 NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_ (X95458) ribosomal protein L39 [Zea mays]

Seq. No. 236973
 Seq. ID uC-gsronu33B019a04b1
 Method BLASTX
 NCBI GI g3201627
 BLAST score 473
 E value 2.0e-47
 Match length 142
 % identity 64
 NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No. 236974
 Seq. ID uC-gsronu33B019b07b1
 Method BLASTX
 NCBI GI g2425129
 BLAST score 234
 E value 1.0e-19
 Match length 92
 % identity 53
 NCBI Description (AF020280) PkgA [Dictyostelium discoideum]

Seq. No. 236975
 Seq. ID uC-gsronu33B019c12b1
 Method BLASTX
 NCBI GI g2213592
 BLAST score 489
 E value 2.0e-49
 Match length 143
 % identity 33
 NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No. 236976
 Seq. ID uC-gsronu33B019d03b1
 Method BLASTX
 NCBI GI g2341024
 BLAST score 177
 E value 8.0e-13
 Match length 118

plumbaginifolia]

Seq. No.	236987
Seq. ID	uC-gsronu33B021c09b1
Method	BLASTX
NCBI GI	g1352681
BLAST score	419
E value	3.0e-41
Match length	128
% identity	65
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir_S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	236988
Seq. ID	uC-gsronu33B021d10b1
Method	BLASTX
NCBI GI	g4558558
BLAST score	445
E value	3.0e-44
Match length	128
% identity	66
NCBI Description	(AC007138) putative polygalacturonidase [Arabidopsis thaliana]
Seq. No.	236989
Seq. ID	uC-gsronu33B021e11b1
Method	BLASTX
NCBI GI	g2062167
BLAST score	205
E value	4.0e-16
Match length	49
% identity	76
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
Seq. No.	236990
Seq. ID	uC-gsronu33B021e12b1
Method	BLASTX
NCBI GI	g3319353
BLAST score	255
E value	4.0e-22
Match length	73
% identity	58
NCBI Description	(AF077407) contains similarity to copper-binding proteins [Arabidopsis thaliana]
Seq. No.	236991
Seq. ID	uC-gsronu33B021f01b1
Method	BLASTX
NCBI GI	g2618686
BLAST score	189
E value	2.0e-14
Match length	89
% identity	40
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

05634016-101000

Seq. No. 236992
 Seq. ID uC-gsronu33B021f02b1
 Method BLASTX
 NCBI GI g3608155
 BLAST score 518
 E value 8.0e-53
 Match length 135
 % identity 68
 NCBI Description (AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No. 236993
 Seq. ID uC-gsronu33B021h11b1
 Method BLASTX
 NCBI GI g2880046
 BLAST score 260
 E value 2.0e-22
 Match length 110
 % identity 55
 NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236994
 Seq. ID uC-gsronu33B027b01b1
 Method BLASTX
 NCBI GI g405080
 BLAST score 148
 E value 1.0e-09
 Match length 101
 % identity 40
 NCBI Description (U01058) ABC family transporter [Entamoeba histolytica]

Seq. No. 236995
 Seq. ID uC-gsronu33B027b09b1
 Method BLASTX
 NCBI GI g2245094
 BLAST score 178
 E value 8.0e-13
 Match length 102
 % identity 43
 NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236996
 Seq. ID uC-gsronu33B027c11b1
 Method BLASTX
 NCBI GI g3256066
 BLAST score 288
 E value 2.0e-37
 Match length 95
 % identity 82
 NCBI Description (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

Seq. No. 236997
 Seq. ID uC-gsronu33B027e04b1
 Method BLASTX
 NCBI GI g2583118
 BLAST score 279
 E value 3.0e-25

E value 2.0e-56
 Match length 147
 % identity 74
 NCBI Description SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150)
 >gi_1173905 (U41371) spliceosome associated protein [Homo sapiens]

Seq. No. 237003
 Seq. ID uC-gsronu33B028c12b1
 Method BLASTX
 NCBI GI g282881
 BLAST score 510
 E value 7.0e-52
 Match length 138
 % identity 67
 NCBI Description receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 237004
 Seq. ID uC-gsronu33B028h03b1
 Method BLASTX
 NCBI GI g2342682
 BLAST score 208
 E value 5.0e-17
 Match length 50
 % identity 74
 NCBI Description (AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No. 237005
 Seq. ID uC-gsronu33B029b10b1
 Method BLASTX
 NCBI GI g3860250
 BLAST score 233
 E value 8.0e-20
 Match length 50
 % identity 90
 NCBI Description (AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No. 237006
 Seq. ID uC-gsronu33B029b11b1
 Method BLASTX
 NCBI GI g4324597
 BLAST score 102
 E value 6.0e-09
 Match length 95
 % identity 45
 NCBI Description (AF106324) sodium proton exchanger Nhxl [Arabidopsis thaliana]

Seq. No. 237007
 Seq. ID uC-gsronu33B029d09b1
 Method BLASTX
 NCBI GI g171366
 BLAST score 253

E value 1.0e-21
 Match length 158
 % identity 35
 NCBI Description (M69294) alantoinase [*Saccharomyces cerevisiae*]

Seq. No. 237008
 Seq. ID uC-gsronu33B029f12b1
 Method BLASTX
 NCBI GI g1184123
 BLAST score 228
 E value 9.0e-19
 Match length 79
 % identity 54
 NCBI Description (U20809) auxin-induced protein [*Vigna radiata*]

Seq. No. 237009
 Seq. ID uC-gsronu33B031a07b1
 Method BLASTX
 NCBI GI g3033377
 BLAST score 410
 E value 4.0e-40
 Match length 137
 % identity 55
 NCBI Description (AC004238) putative berberine bridge enzyme [*Arabidopsis thaliana*]

Seq. No. 237010
 Seq. ID uC-gsronu33B031b03b1
 Method BLASTX
 NCBI GI g4103635
 BLAST score 328
 E value 2.0e-30
 Match length 94
 % identity 64
 NCBI Description (AF026538) ABA-responsive protein [*Hordeum vulgare*]

Seq. No. 237011
 Seq. ID uC-gsronu33B031b10b1
 Method BLASTX
 NCBI GI g3549660
 BLAST score 341
 E value 5.0e-32
 Match length 123
 % identity 56
 NCBI Description (AL031394) carbonate dehydratase - like protein [*Arabidopsis thaliana*]

Seq. No. 237012
 Seq. ID uC-gsronu33B031e03b1
 Method BLASTX
 NCBI GI g2738949
 BLAST score 290
 E value 3.0e-26
 Match length 90
 % identity 66
 NCBI Description (AF022213) cytosolic ascorbate peroxidase [*Fragaria x ananassa*]

Seq. No. 237013
 Seq. ID uC-gsronu33B031g01b1
 Method BLASTX
 NCBI GI g2384760
 BLAST score 189
 E value 2.0e-14
 Match length 47
 % identity 74
 NCBI Description (AF016897) GDP dissociation inhibitor protein OsgDI2 [Oryza sativa]

Seq. No. 237014
 Seq. ID uC-gsronu33B031g08b1
 Method BLASTX
 NCBI GI g3548802
 BLAST score 185
 E value 3.0e-14
 Match length 53
 % identity 64
 NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]
 >gi_4335769_gb_AAD17446_ (AC006284) putative axil protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 237015
 Seq. ID uC-gsronu33B031h06b1
 Method BLASTX
 NCBI GI g3402704
 BLAST score 469
 E value 6.0e-47
 Match length 138
 % identity 74
 NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237016
 Seq. ID uC-gsronu33B032c03b1
 Method BLASTX
 NCBI GI g3461846
 BLAST score 300
 E value 1.0e-27
 Match length 84
 % identity 36
 NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No. 237017
 Seq. ID uC-gsronu33B032g02b1
 Method BLASTX
 NCBI GI g2129742
 BLAST score 275
 E value 3.0e-24
 Match length 77
 % identity 65
 NCBI Description stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related

Method BLASTX
 NCBI GI g2253583
 BLAST score 294
 E value 1.0e-26
 Match length 96
 % identity 66
 NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237024
 Seq. ID uC-gsronu33B036f08b1
 Method BLASTX
 NCBI GI g2443887
 BLAST score 614
 E value 5.0e-64
 Match length 152
 % identity 76
 NCBI Description (AC002294) Similar to transcription factor gb_246606_1658307 and others [Arabidopsis thaliana]

Seq. No. 237025
 Seq. ID uC-gsronu33B036h01b1
 Method BLASTX
 NCBI GI g1170409
 BLAST score 188
 E value 4.0e-14
 Match length 61
 % identity 67
 NCBI Description HOMEBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) >gi_549887 (U09336) homeobox protein [Arabidopsis thaliana] >gi_549888 (U09337) homeobox protein [Arabidopsis thaliana] >gi_4490724_emb_CAB38927.1_ (AL035709) homeobox protein HAT22 [Arabidopsis thaliana]

Seq. No. 237026
 Seq. ID uC-gsronu33B037b05b1
 Method BLASTX
 NCBI GI g881625
 BLAST score 319
 E value 2.0e-29
 Match length 70
 % identity 80
 NCBI Description (U29432) 22.8 kDa protein [Ipomoea trifida]

Seq. No. 237027
 Seq. ID uC-gsronu33B037b06b1
 Method BLASTX
 NCBI GI g1076685
 BLAST score 358
 E value 3.0e-34
 Match length 103
 % identity 44
 NCBI Description SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_ (D30038) SPF1 protein [Ipomoea batatas]

Seq. No. 237028
 Seq. ID uC-gsronu33B037b10b1
 Method BLASTX

NCBI GI g3738089
 BLAST score 231
 E value 2.0e-19
 Match length 86
 % identity 59
 NCBI Description (AC005617) similar to symbiotic ammonium transporter, SAT1 [Arabidopsis thaliana] >gi_4314372_gb_AAD15583_ (AC006340) putative symbiotic ammonium transporter SAT1 [Arabidopsis thaliana]

Seq. No. 237029
 Seq. ID uC-gsronu33B037c09b1
 Method BLASTX
 NCBI GI g4263722
 BLAST score 312
 E value 5.0e-29
 Match length 90
 % identity 67
 NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 237030
 Seq. ID uC-gsronu33B037f01b1
 Method BLASTX
 NCBI GI g3033380
 BLAST score 430
 E value 1.0e-42
 Match length 102
 % identity 80
 NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No. 237031
 Seq. ID uC-gsronu33B037f05b1
 Method BLASTX
 NCBI GI g3953471
 BLAST score 222
 E value 3.0e-18
 Match length 53
 % identity 70
 NCBI Description (AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No. 237032
 Seq. ID uC-gsronu33B037f12b1
 Method BLASTX
 NCBI GI g3548802
 BLAST score 372
 E value 1.0e-35
 Match length 141
 % identity 51
 NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axil protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 237033
 Seq. ID uC-gsronu33B037g07b1
 Method BLASTX
 NCBI GI g3986110

NCBI Description (AF003197) glutamine synthetase [Hevea brasiliensis]

Seq. No. 237039
Seq. ID uC-gsronu33B038e03b1
Method BLASTX
NCBI GI g1938424
BLAST score 267
E value 2.0e-23
Match length 148
% identity 39

NCBI Description (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]

Seq. No. 237040
Seq. ID uC-gsronu33B038e09b1
Method BLASTX
NCBI GI g3600033
BLAST score 475
E value 1.0e-47
Match length 168
% identity 54

NCBI Description (AF080119) contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana]

Seq. No. 237041
Seq. ID uC-gsronu33B038e11b1
Method BLASTX
NCBI GI g2244868
BLAST score 562
E value 6.0e-58
Match length 115
% identity 89
NCBI Description (Z97337) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 237042
Seq. ID uC-gsronu33B038f12b1
Method BLASTX
NCBI GI g4566614
BLAST score 186
E value 3.0e-14
Match length 47
% identity 77
NCBI Description (AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No. 237043
Seq. ID uC-gsronu33B038g07b1
Method BLASTX
NCBI GI g3096922
BLAST score 293
E value 2.0e-26
Match length 84
% identity 69
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 237044

Seq. ID uC-gsronu33B038h03b1
 Method BLASTX
 NCBI GI g2262113
 BLAST score 238
 E value 6.0e-20
 Match length 74
 % identity 72
 NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 237045
 Seq. ID uC-gsronu33B038h10b1
 Method BLASTX
 NCBI GI g1297187
 BLAST score 568
 E value 1.0e-58
 Match length 162
 % identity 69
 NCBI Description (U53501) similar to protein encoded by GenBank Accession Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No. 237046
 Seq. ID uC-gsronu33B039f07b1
 Method BLASTX
 NCBI GI g3860256
 BLAST score 358
 E value 2.0e-34
 Match length 91
 % identity 71
 NCBI Description (AC005824) putative tRNA isopentenylpyrophosphate transferase [Arabidopsis thaliana]

Seq. No. 237047
 Seq. ID uC-gsronu33B039h03b1
 Method BLASTX
 NCBI GI g4335729
 BLAST score 201
 E value 8.0e-16
 Match length 108
 % identity 5
 NCBI Description (AC006248) putative salt-inducible protein [Arabidopsis thaliana]

Seq. No. 237048
 Seq. ID uC-gsronu33B040a09b1
 Method BLASTX
 NCBI GI g2459435
 BLAST score 144
 E value 2.0e-09
 Match length 42
 % identity 62
 NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 237049
 Seq. ID uC-gsronu33B040b01b1
 Method BLASTX
 NCBI GI g3395436

BLAST score 154
 E value 5.0e-10
 Match length 123
 % identity 32
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 237050
 Seq. ID uC-gsronu33B040c05b1
 Method BLASTX
 NCBI GI g4566505
 BLAST score 190
 E value 9.0e-15
 Match length 67
 % identity 55
 NCBI Description (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No. 237051
 Seq. ID uC-gsronu33B040f01b1
 Method BLASTX
 NCBI GI g2911042
 BLAST score 459
 E value 6.0e-46
 Match length 129
 % identity 74
 NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No. 237052
 Seq. ID uC-gsronu33B041a01b1
 Method BLASTX
 NCBI GI g3023194
 BLAST score 644
 E value 2.0e-67
 Match length 134
 % identity 95
 NCBI Description 14-3-3-LIKE PROTEIN A (SGF14A) >gi_1575725 (U70533) SGF14A [Glycine max]

Seq. No. 237053
 Seq. ID uC-gsronu33B041e03b1
 Method BLASTX
 NCBI GI g3335362
 BLAST score 167
 E value 1.0e-11
 Match length 57
 % identity 54
 NCBI Description (AC003028) putative ribosomal protein S31 [Arabidopsis thaliana]

Seq. No. 237054
 Seq. ID uC-gsronu33B041g06b1
 Method BLASTX
 NCBI GI g2245131
 BLAST score 212
 E value 4.0e-17
 Match length 74

% identity 61
NCBI Description (297344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237055
Seq. ID uC-gsronu33B041h07b1
Method BLASTX
NCBI GI g3850823
BLAST score 190
E value 7.0e-15
Match length 70
% identity 56
NCBI Description (Y18351) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]

Seq. No. 237056
Seq. ID uC-gsronu33B041h09b1
Method BLASTX
NCBI GI g1173218
BLAST score 326
E value 2.0e-30
Match length 62
% identity 100
NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 237057
Seq. ID uC-gsronu33B042d02b1
Method BLASTX
NCBI GI g3510505
BLAST score 307
E value 4.0e-28
Match length 130
% identity 44
NCBI Description (AF030881) pol polyprotein [Fugu rubripes]

Seq. No. 237058
Seq. ID uC-gsronu33B042e04b1
Method BLASTX
NCBI GI g3924603
BLAST score 307
E value 1.0e-28
Match length 76
% identity 53
NCBI Description (AF069442) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No. 237059
Seq. ID uC-gsronu33B042f03b1
Method BLASTX
NCBI GI g417540
BLAST score 388
E value 2.0e-37
Match length 117
% identity 67
NCBI Description PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi_20851_emb_CAA44646_ (X62842) pyrroline carboxylate


```
Seq. No.      237065
Seq. ID       uC-gsronu33B044e12b1
Method        BLASTX
NCBI GI       g1173209
BLAST score    600
E value       2.0e-62
Match length   120
% identity     99
NCBI Description  40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
                  protein S16 protein - upland cotton
                  >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                  [Gossypium hirsutum]
```

```
Seq. No.      237066
Seq. ID       uC-gsronu33B044g05b1
Method        BLASTX
NCBI GI       g2335101
BLAST score   523
E value       2.0e-53
Match length  117
% identity    79
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]
```

Seq. No.	237067
Seq. ID	uC-gsronu33B046a03b1
Method	BLASTX
NCBI GI	g2465923
BLAST score	474
E value	1.0e-47
Match length	122
% identity	73
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

```
Seq. No.      237068
Seq. ID       uC-gsronu33B046c04b1
Method        BLASTX
NCBI GI       g1076275
BLAST score    202
E value       2.0e-16
Match length   43
% identity     93
NCBI Description phenylalanine ammonia-lyase - muskmelon
                >gi_735957_emb_CAA53733_ (X76130) phenylalanine
                ammonia-lyase [Cucumis melo]
```

```
Seq. No.          237069
Seq. ID           uC-gsronu33B046c07b1
Method            BLASTX
NCBI GI           g2739279
BLAST score       170
E value           4.0e-12
Match length      77
% identity        43
NCBI Description   (AJ223177) short chain alcohol dehydrogenase [Nicotiana
                  tabacum] >gi_2791348_emb_CAA11154_(AJ223178) short chain
                  alcohol dehydrogenase [Nicotiana tabacum]
```


E value 2.0e-27
 Match length 102
 % identity 59
 NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 237076
 Seq. ID uC-gsronu33B047b02b1
 Method BLASTX
 NCBI GI g2493852
 BLAST score 291
 E value 4.0e-26
 Match length 63
 % identity 84
 NCBI Description CYTOCHROME C OXIDASE POLYPEPTIDE VC
 >gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc subunit [Hordeum vulgare]

Seq. No. 237077
 Seq. ID uC-gsronu33B047b08b1
 Method BLASTX
 NCBI GI g2760327
 BLAST score 498
 E value 1.0e-50
 Match length 109
 % identity 44
 NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No. 237078
 Seq. ID uC-gsronu33B047e03b1
 Method BLASTX
 NCBI GI g1076793
 BLAST score 638
 E value 7.0e-67
 Match length 138
 % identity 62
 NCBI Description calmodulin, cam2 - maize >gi_747917_emb_CAA54583_ (X77397)
 calmodulin [Zea mays]

Seq. No. 237079
 Seq. ID uC-gsronu33B047f02b1
 Method BLASTX
 NCBI GI g2626753
 BLAST score 522
 E value 4.0e-53
 Match length 168
 % identity 65
 NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No. 237080
 Seq. ID uC-gsronu33B048b01b1
 Method BLASTX
 NCBI GI g4538911
 BLAST score 180
 E value 3.0e-13
 Match length 119
 % identity 32

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237081
Seq. ID uC-gsronu33B048e02b1
Method BLASTX
NCBI GI g2244749
BLAST score 499
E value 8.0e-51
Match length 98
% identity 94

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 237082
Seq. ID uC-gsronu33B048e05b1
Method BLASTX
NCBI GI g2098705
BLAST score 534
E value 1.0e-56
Match length 153
% identity 77

NCBI Description (U82973) pectinesterase [Citrus sinensis]

Seq. No. 237083
Seq. ID uC-gsronu33B048e08b1
Method BLASTX
NCBI GI g2244949
BLAST score 265
E value 2.0e-23
Match length 72
% identity 75

NCBI Description (Z97339) similarity to ORF - Lilium longiflorum [Arabidopsis thaliana]

Seq. No. 237084
Seq. ID uC-gsronu33B048e12b1
Method BLASTX
NCBI GI g2078350
BLAST score 212
E value 5.0e-17
Match length 108
% identity 44

NCBI Description (U95923) transaldolase [Solanum tuberosum]

Seq. No. 237085
Seq. ID uC-gsronu33B048g02b1
Method BLASTX
NCBI GI g3687389
BLAST score 339
E value 3.0e-32
Match length 78
% identity 85

NCBI Description (Y16124) putative cullin protein [Lycopersicon esculentum]

Seq. No. 237086
Seq. ID uC-gsronu33B049a03b1
Method BLASTX
NCBI GI g4469025

Seq. No. 237103
 Seq. ID uC-gsronu33B055d07b1
 Method BLASTX
 NCBI GI g4049401
 BLAST score 185
 E value 5.0e-14
 Match length 51
 % identity 67
 NCBI Description (AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]

Seq. No. 237104
 Seq. ID uC-gsronu33B055d09b1
 Method BLASTX
 NCBI GI g1169200
 BLAST score 313
 E value 2.0e-29
 Match length 73
 % identity 79
 NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR >gi_421829_pir_S33706 DNA-damage resistance protein - Arabidopsis thaliana >gi_166694 (M98455) [Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT111) mRNA, complete cds.], gene product [Arabidopsis thaliana]

Seq. No. 237105
 Seq. ID uC-gsronu33B055e08b1
 Method BLASTX
 NCBI GI g1019946
 BLAST score 149
 E value 4.0e-10
 Match length 33
 % identity 82
 NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]

Seq. No. 237106
 Seq. ID uC-gsronu33B055f08b1
 Method BLASTX
 NCBI GI g730456
 BLAST score 309
 E value 1.0e-28
 Match length 68
 % identity 81
 NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 237107
 Seq. ID uC-gsronu33B055h04b1
 Method BLASTX
 NCBI GI g4468805
 BLAST score 256
 E value 2.0e-22
 Match length 84
 % identity 56
 NCBI Description (AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No. 237108
 Seq. ID uC-gsronu33B057a11b1
 Method BLASTX
 NCBI GI g2224897
 BLAST score 275
 E value 2.0e-24
 Match length 118
 % identity 53
 NCBI Description (U67132) DNA-binding protein PcMYB1 [Petroselinum crispum]

Seq. No. 237109
 Seq. ID uC-gsronu33B057b08b1
 Method BLASTX
 NCBI GI g2984292
 BLAST score 184
 E value 2.0e-17
 Match length 108
 % identity 48
 NCBI Description (AE000771) GTP-binding protein [Aquifex aeolicus]

Seq. No. 237110
 Seq. ID uC-gsronu33B057d12b1
 Method BLASTX
 NCBI GI g4539348
 BLAST score 136
 E value 1.0e-17
 Match length 95
 % identity 52
 NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No. 237111
 Seq. ID uC-gsronu33B057f05b1
 Method BLASTX
 NCBI GI g4510345
 BLAST score 222
 E value 1.0e-18
 Match length 48
 % identity 81
 NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 237112
 Seq. ID uC-gsronu33B057g04b1
 Method BLASTX
 NCBI GI g1352186
 BLAST score 325
 E value 2.0e-30
 Match length 89
 % identity 70
 NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 237113
 Seq. ID uC-gsronu33B057g08b1
 Method BLASTX
 NCBI GI g529353

NCBI GI g4262236
 BLAST score 151
 E value 3.0e-10
 Match length 57
 % identity 61
 NCBI Description (AC006200) putative ribose 5-phosphate isomerase
 [Arabidopsis thaliana]

Seq. No. 237125
 Seq. ID uC-gsronu33B060c07b1
 Method BLASTX
 NCBI GI g441457
 BLAST score 178
 E value 3.0e-22
 Match length 74
 % identity 78
 NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
 esculentum]

Seq. No. 237126
 Seq. ID uC-gsronu33B061a01b1
 Method BLASTX
 NCBI GI g2495256
 BLAST score 616
 E value 3.0e-64
 Match length 137
 % identity 82
 NCBI Description STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG
 PROTEIN) >gi_481756_pir_S39242 HMG protein - Madagascar
 periwinkle >gi_433872_emb_CAA82251_ (Z28410) HMG protein
 [Catharanthus roseus]

Seq. No. 237127
 Seq. ID uC-gsronu33B061a08b1
 Method BLASTX
 NCBI GI g3915961
 BLAST score 564
 E value 3.0e-58
 Match length 124
 % identity 90
 NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
 >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana
 tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
 protein [Nicotiana tabacum]

Seq. No. 237128
 Seq. ID uC-gsronu33B061b06b1
 Method BLASTX
 NCBI GI g2129772
 BLAST score 173
 E value 1.0e-12
 Match length 39
 % identity 74
 NCBI Description xyloglucan endotransglycosylase-related protein XTR-7 -
 Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan
 endotransglycosylase-related protein [Arabidopsis thaliana]

NCBI Description 14-3-3-LIKE PROTEIN A (SGF14A) >gi_1575725 (U70533) SGF14A
[Glycine max]

Seq. No. 237140
Seq. ID uC-gsronu33B072c10b1
Method BLASTX
NCBI GI g3776559
BLAST score 220
E value 2.0e-18
Match length 57
% identity 70

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933
cdc2 protein kinase homolog from A. thaliana BAC
gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
gene. [Arabidopsis thaliana]

Seq. No. 237141
Seq. ID uC-gsronu33B074a06b1
Method BLASTX
NCBI GI g1171577
BLAST score 138
E value 7.0e-09
Match length 41
% identity 68

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 237142
Seq. ID uC-gsronu33B074f02b1
Method BLASTX
NCBI GI g2914700
BLAST score 147
E value 6.0e-10
Match length 46
% identity 67

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
thaliana]

Seq. No. 237143
Seq. ID uC-gsronu33B076a02b1
Method BLASTX
NCBI GI g3004547
BLAST score 153
E value 3.0e-10
Match length 35
% identity 86

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]
>gi_4185150 (AC005724) unknown protein [Arabidopsis
thaliana]

Seq. No. 237144
Seq. ID uC-gsronu33B076a04b1
Method BLASTX
NCBI GI g2500649
BLAST score 210
E value 5.0e-17
Match length 87
% identity 47

NCBI Description PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE
(RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)

Seq. No. 237145
Seq. ID uC-gsronu33B076c03b1
Method BLASTX
NCBI GI g1469930
BLAST score 181
E value 1.0e-13
Match length 45
% identity 82
NCBI Description (U48777) fiber-specific acyl carrier protein [Gossypium
hirsutum]

Seq. No. 237146
Seq. ID uC-gsronu33B076c12b1
Method BLASTX
NCBI GI g548770
BLAST score 159
E value 4.0e-11
Match length 36
% identity 83
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal
protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
ribosomal protein L3 [Oryza sativa]

Seq. No. 237147
Seq. ID uC-gsronu33B076f02b1
Method BLASTX
NCBI GI g3098571
BLAST score 232
E value 2.0e-19
Match length 82
% identity 51
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]

Seq. No. 237148
Seq. ID uC-gsronu33B076g03b1
Method BLASTX
NCBI GI g3193234
BLAST score 156
E value 2.0e-10
Match length 43
% identity 67
NCBI Description (AF068690) peroxisomal targeting signal-1 receptor
[Citrullus lanatus]

Seq. No. 237149
Seq. ID uC-gsronu33B077a08b1
Method BLASTX
NCBI GI g2058280
BLAST score 198
E value 7.0e-16
Match length 37
% identity 97
NCBI Description (X97381) atran3 [Arabidopsis thaliana]

Seq. No. 237150
 Seq. ID uC-gsronu33B077b04b1
 Method BLASTX
 NCBI GI g4415908
 BLAST score 420
 E value 2.0e-41
 Match length 110
 % identity 65
 NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 237151
 Seq. ID uC-gsronu33B077c01b1
 Method BLASTX
 NCBI GI g1620371
 BLAST score 511
 E value 6.0e-52
 Match length 118
 % identity 77
 NCBI Description (Y08782) peroxidase ATP23a [Arabidopsis thaliana]

Seq. No. 237152
 Seq. ID uC-gsronu33B077c10b1
 Method BLASTX
 NCBI GI g4038030
 BLAST score 441
 E value 1.0e-43
 Match length 125
 % identity 63
 NCBI Description (AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No. 237153
 Seq. ID uC-gsronu33B077c12b1
 Method BLASTX
 NCBI GI g3242717
 BLAST score 400
 E value 4.0e-39
 Match length 93
 % identity 81
 NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No. 237154
 Seq. ID uC-gsronu33B077e04b1
 Method BLASTX
 NCBI GI g3269301
 BLAST score 516
 E value 1.0e-52
 Match length 143
 % identity 63
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 237155
 Seq. ID uC-gsronu33B077e11b1
 Method BLASTX
 NCBI GI g1171579
 BLAST score 250
 E value 2.0e-21

>gi_2267583 (AF009338) vacuolar H⁺-ATPase subunit E
[Gossypium hirsutum]

Seq. No. 237161
Seq. ID uC-gsronu33B078a10b1
Method BLASTX
NCBI GI g2833390
BLAST score 367
E value 2.0e-35
Match length 80
% identity 80
NCBI Description GLYCOGEN (STARCH) SYNTHASE PRECURSOR (GBSSII)
(GRANULE-BOUND STARCH SYNTHASE II) >gi_887649_emb_CAA61241_
(X87988) glycogen (starch) synthase [Solanum tuberosum]

Seq. No. 237162
Seq. ID uC-gsronu33B078b12b1
Method BLASTX
NCBI GI g1669601
BLAST score 541
E value 2.0e-55
Match length 149
% identity 67
NCBI Description (D88747) AR401 [Arabidopsis thaliana]

Seq. No. 237163
Seq. ID uC-gsronu33B078c02b1
Method BLASTX
NCBI GI g3811293
BLAST score 149
E value 2.0e-09
Match length 55
% identity 64
NCBI Description (AF032465) putative serine/threonine protein kinase
[Nicotiana tabacum] >gi_4098172 (U73938) PK11-C1 [Nicotiana
tabacum]

Seq. No. 237164
Seq. ID uC-gsronu33B078c06b1
Method BLASTX
NCBI GI g1523800
BLAST score 340
E value 4.0e-32
Match length 103
% identity 56
NCBI Description (Y07694) MAP kinase kinase alpha protein kinase
[Arabidopsis thaliana]

Seq. No. 237165
Seq. ID uC-gsronu33B078c07b1
Method BLASTX
NCBI GI g3176715
BLAST score 504
E value 4.0e-51
Match length 114
% identity 83
NCBI Description (AC002392) putative receptor-like protein kinase

Seq. No. 237191
 Seq. ID uC-gsronu33B080e11b1
 Method BLASTX
 NCBI GI g3158474
 BLAST score 635
 E value 2.0e-66
 Match length 137
 % identity 89
 NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 237192
 Seq. ID uC-gsronu33B080e12b1
 Method BLASTX
 NCBI GI g3355468
 BLAST score 522
 E value 3.0e-53
 Match length 120
 % identity 89
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 237193
 Seq. ID uC-gsronu33B080f12b1
 Method BLASTX
 NCBI GI g4559346
 BLAST score 242
 E value 2.0e-20
 Match length 91
 % identity 45
 NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No. 237194
 Seq. ID uC-gsronu33B080g03b1
 Method BLASTX
 NCBI GI g1563719
 BLAST score 324
 E value 4.0e-30
 Match length 68
 % identity 88
 NCBI Description (Y08320) cyclophylin [Digitalis lanata]

Seq. No. 237195
 Seq. ID uC-gsronu33B080h03b1
 Method BLASTX
 NCBI GI g4572679
 BLAST score 280
 E value 3.0e-25
 Match length 71
 % identity 77
 NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 237196
 Seq. ID uC-gsronu33B080h08b1
 Method BLASTX
 NCBI GI g3850816
 BLAST score 235

E value 6.0e-22
 Match length 144
 % identity 39
 NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 237207
 Seq. ID uC-gsronu33B082c10b1
 Method BLASTX
 NCBI GI g2979544
 BLAST score 369
 E value 2.0e-35
 Match length 108
 % identity 64
 NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No. 237208
 Seq. ID uC-gsronu33B082d11b1
 Method BLASTX
 NCBI GI g3420906
 BLAST score 364
 E value 1.0e-34
 Match length 112
 % identity 41
 NCBI Description (AF080595) zinc finger protein; WRKY1 [Pimpinella
 brachycarpa]

Seq. No. 237209
 Seq. ID uC-gsronu33B082f08b1
 Method BLASTX
 NCBI GI g1518540
 BLAST score 838
 E value 3.0e-90
 Match length 167
 % identity 92
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 237210
 Seq. ID uC-gsronu33B082f10b1
 Method BLASTX
 NCBI GI g3858935
 BLAST score 243
 E value 1.0e-20
 Match length 83
 % identity 58
 NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis
 thaliana] >gi_4103357 (AF025332) vesicle-associated
 membrane protein 7C; synaptobrevin 7C [Arabidopsis
 thaliana]

Seq. No. 237211
 Seq. ID uC-gsronu33B082h12b1
 Method BLASTX
 NCBI GI g2252847
 BLAST score 161
 E value 3.0e-11
 Match length 84
 % identity 42

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 237212
Seq. ID uC-gsronu33B086d12b1
Method BLASTX
NCBI GI g4185819
BLAST score 192
E value 5.0e-15
Match length 47
% identity 68

NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No. 237213
Seq. ID uC-gsronu33B086e02b1
Method BLASTX
NCBI GI g2959781
BLAST score 180
E value 9.0e-14
Match length 39
% identity 87

NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 237214
Seq. ID uC-gsronu33B086g12b1
Method BLASTX
NCBI GI g2244898
BLAST score 220
E value 2.0e-18
Match length 45
% identity 96
NCBI Description (Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 237215
Seq. ID uC-gsronu33B086h10b1
Method BLASTX
NCBI GI g99749
BLAST score 204
E value 1.0e-16
Match length 38
% identity 95
NCBI Description probable serine/threonine-specific protein kinase ATPK64 (EC 2.7.1.-) - Arabidopsis thaliana
>gi_217843_dbj_BAA01731_ (D10937) protein kinase [Arabidopsis thaliana]

Seq. No. 237216
Seq. ID uC-gsronu33B087c05b1
Method BLASTX
NCBI GI g4008072
BLAST score 164
E value 1.0e-11
Match length 66
% identity 45
NCBI Description (AF105425) chitinase [Cynodon dactylon]

Seq. No. 237217
 Seq. ID uC-gsronu33B087f01b1
 Method BLASTX
 NCBI GI g1168408
 BLAST score 161
 E value 2.0e-11
 Match length 38
 % identity 82
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
 >gi_2118268_pir_S58168 fructose-bisphosphate aldolase (EC
 4.1.2.13) - garden pea >gi_927507_emb_CAA61946_ (X89828)
 fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 237218
 Seq. ID uC-gsronu33B087f08b1
 Method BLASTX
 NCBI GI g3420008
 BLAST score 238
 E value 5.0e-20
 Match length 106
 % identity 42
 NCBI Description (AF000307) steroid sulfotransferase 3 [Brassica napus]

Seq. No. 237219
 Seq. ID uC-gsronu33B087h07b1
 Method BLASTX
 NCBI GI g3482929
 BLAST score 147
 E value 9.0e-10
 Match length 28
 % identity 93
 NCBI Description (AC003970) Putative transcription factor [Arabidopsis
 thaliana]

Seq. No. 237220
 Seq. ID uC-gsronu33B089b08b1
 Method BLASTX
 NCBI GI g2462828
 BLAST score 247
 E value 2.0e-21
 Match length 87
 % identity 53
 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237221
 Seq. ID uC-gsronu33B089b11b1
 Method BLASTX
 NCBI GI g4115377
 BLAST score 169
 E value 6.0e-12
 Match length 53
 % identity 75
 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 237222
 Seq. ID uC-gsronu33B089c05b1
 Method BLASTX

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NCBI GI g416650
BLAST score 400
E value 6.0e-39
Match length 112
% identity 68
NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT35/PCNT111) >gi_100304_pir_S16268 auxin-induced protein (clone pGNT35) - common tobacco
>gi_19797_emb_CAA39706_ (X56265) auxin-induced protein [Nicotiana tabacum] >gi_19801_emb_CAA39710_ (X56269) auxin-induced protein [Nicotiana tabacum]

Seq. No. 237223
Seq. ID uC-gsronu33B089d08b1
Method BLASTX
NCBI GI g3395440
BLAST score 339
E value 1.0e-44
Match length 135
% identity 64
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237224
Seq. ID uC-gsronu33B089e01b1
Method BLASTX
NCBI GI g1168470
BLAST score 570
E value 6.0e-59
Match length 121
% identity 89
NCBI Description PROTEIN KINASE APK1A >gi_282877_pir_S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No. 237225
Seq. ID uC-gsronu33B089f09b1
Method BLASTX
NCBI GI g1946329
BLAST score 446
E value 2.0e-44
Match length 123
% identity 68
NCBI Description (U69154) prohibitin [Nicotiana tabacum]

Seq. No. 237226
Seq. ID uC-gsronu33B089h12b1
Method BLASTX
NCBI GI g125606
BLAST score 141
E value 8.0e-09
Match length 55
% identity 56
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir_S12248 pyruvate kinase (EC 2.7.1.40) - potato
>gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum

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Seq. No.      237228
Seq. ID       uC-gsronu33B090e06b1
Method        BLASTX
NCBI GI       g2909781
BLAST score   261
E value       1.0e-22
Match length  120
% identity    47
NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump
[Arabidopsis thaliana]
```

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Seq. No.      237229
Seq. ID       uC-gsronu33B090e07b1
Method        BLASTX
NCBI GI       g4512698
BLAST score   325
E value       4.0e-30
Match length  150
% identity    39
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
```

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Seq. No.      237230
Seq. ID       uC-gsronu33B090f06b1
Method        BLASTX
NCBI GI       g4056456
BLAST score   177
E value       8.0e-13
Match length  101
% identity    46
NCBI Description (AC005990) Strong similarity to gb_U20808 auxin-induced
protein from Vigna radiata and a member of the zinc-binding
dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006
and gb_AA395179 come from this gene. [Arabidopsis thaliana]
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Seq. No.          237231
Seq. ID          uC-gsronu33B096e09b1
Method           BLASTX
NCBI GI          g3033397
BLAST score      136
E value          1.0e-08
Match length     26
% identity       88
NCBI Description  (AC004238) unknown protein [Arabidopsis thaliana]
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Seq. No.	237232
Seq. ID	uC-gsronu33B096g02b1
Method	BLASTX
NCBI GI	g3860250
BLAST score	543
E value	7.0e-56
Match length	118
% identity	89
NCBI Description	(AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]
Seq. No.	237233
Seq. ID	uC-gsronu33B098a02b1
Method	BLASTX
NCBI GI	g1168727
BLAST score	167
E value	5.0e-12
Match length	42
% identity	86
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol dehydrogenase [Aralia cordata] >gi_745086_prf_2015401A cinnamoyl alcohol dehydrogenase [Aralia cordata]
Seq. No.	237234
Seq. ID	uC-gsronu33B098a04b1
Method	BLASTX
NCBI GI	g1076609
BLAST score	243
E value	8.0e-21
Match length	50
% identity	86
NCBI Description	NTL1 protein - curled-leaved tobacco
Seq. No.	237235
Seq. ID	uC-gsronu33B098a11b1
Method	BLASTX
NCBI GI	g4455159
BLAST score	283
E value	3.0e-32
Match length	86
% identity	79
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]
Seq. No.	237236
Seq. ID	uC-gsronu33B098e05b1
Method	BLASTX
NCBI GI	g4158219
BLAST score	484
E value	8.0e-49
Match length	138
% identity	67
NCBI Description	(Y18623) amylogenin [Oryza sativa]
Seq. No.	237237
Seq. ID	uC-gsronu33B098h04b1
Method	BLASTX

NCBI GI g2765748
 BLAST score 180
 E value 3.0e-13
 Match length 41
 % identity 85
 NCBI Description (Z93764) PaMip-2 [Picea abies]

Seq. No. 237238
 Seq. ID uC-gsronu33B099a06b1
 Method BLASTX
 NCBI GI g1915974
 BLAST score 160
 E value 3.0e-11
 Match length 45
 % identity 71
 NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >gi_2102693
 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No. 237239
 Seq. ID uC-gsronu33B099a07b1
 Method BLASTX
 NCBI GI g3193310
 BLAST score 303
 E value 1.0e-27
 Match length 113
 % identity 55
 NCBI Description (AF069300) contains similarity to Nicotiana tabacum hin1
 (GB:Y07563) [Arabidopsis thaliana]

Seq. No. 237240
 Seq. ID uC-gsronu33B099b08b1
 Method BLASTX
 NCBI GI g1084455
 BLAST score 170
 E value 2.0e-12
 Match length 38
 % identity 89
 NCBI Description peptidylprolyl isomerase (EC 5.2.1.8). Cyp2 - rice
 >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No. 237241
 Seq. ID uC-gsronu33B099c03b1
 Method BLASTX
 NCBI GI g3142300
 BLAST score 389
 E value 1.0e-37
 Match length 118
 % identity 64
 NCBI Description (AC002411) Contains similarity to pre-mRNA processing
 protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
 and gb_T88158, gb_N38703 and gb_AA651043 come from this
 gene. [Arabidopsis thaliana]

Seq. No. 237242
 Seq. ID uC-gsronu33B099c09b1
 Method BLASTX
 NCBI GI g2811025

BLAST score 612
 E value 7.0e-64
 Match length 136
 % identity 82
 NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
 (AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 237243
 Seq. ID uC-gsronu33B099d02b1
 Method BLASTX
 NCBI GI g4200165
 BLAST score 721
 E value 1.0e-76
 Match length 145
 % identity 86
 NCBI Description (Y16262) neutral invertase [Daucus carota]

Seq. No. 237244
 Seq. ID uC-gsronu33B099d05b1
 Method BLASTX
 NCBI GI g3540207
 BLAST score 344
 E value 2.0e-32
 Match length 102
 % identity 71
 NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 237245
 Seq. ID uC-gsronu33B099d10b1
 Method BLASTX
 NCBI GI g642339
 BLAST score 199
 E value 2.0e-15
 Match length 99
 % identity 47
 NCBI Description (X83226) peroxisome biogenesis invlved proteind
 [Saccharomyces cerevisiae]

Seq. No. 237246
 Seq. ID uC-gsronu33B099e07b1
 Method BLASTX
 NCBI GI g1172571
 BLAST score 517
 E value 9.0e-53
 Match length 126
 % identity 97
 NCBI Description PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
 >gi_1076277_pir_S52637 phosphoenolpyruvate carboxykinase
 (ATP) (EC 4.1.1.49) - cucumber >gi_567102 (L31899)
 phosphoenolpyruvate carboxykinase [Cucumis sativus]

Seq. No. 237247
 Seq. ID uC-gsronu33B099e11b1
 Method BLASTX
 NCBI GI g2632105
 BLAST score 586
 E value 9.0e-61

Match length 121
% identity 68
NCBI Description (AB013912) DNA helicase [Mus musculus]

Seq. No. 237258
Seq. ID uC-gsronu33B100g05b1
Method BLASTX
NCBI GI g2462751
BLAST score 168
E value 4.0e-12
Match length 36
% identity 92
NCBI Description (AC002292) nearly identical to rice water stress induced protein gp_D26537_537404 [Arabidopsis thaliana]

Seq. No. 237259
Seq. ID uC-gsronu33B100g12b1
Method BLASTX
NCBI GI g2911799
BLAST score 214
E value 9.0e-18
Match length 48
% identity 90
NCBI Description (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No. 237260
Seq. ID uC-gsronu33B101a03b1
Method BLASTX
NCBI GI g4038035
BLAST score 231
E value 9.0e-20
Match length 60
% identity 82
NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No. 237261
Seq. ID uC-gsronu33B101f02b1
Method BLASTX
NCBI GI g4567312
BLAST score 464
E value 1.0e-46
Match length 113
% identity 75
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237262
Seq. ID uC-gsronu33B103a02b1
Method BLASTX
NCBI GI g3164115
BLAST score 228
E value 7.0e-19
Match length 114
% identity 40
NCBI Description (AJ224145) major latex-like protein [Rubus idaeus]

Seq. No.	237263
Seq. ID	uC-gsronu33B103b01b1
Method	BLASTX
NCBI GI	g2244876
BLAST score	363
E value	1.0e-34
Match length	93
% identity	70
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237264
Seq. ID	uC-gsronu33B103d06b1
Method	BLASTX
NCBI GI	g2464901
BLAST score	211
E value	4.0e-17
Match length	86
% identity	47
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	237265
Seq. ID	uC-gsronu33B103d07b1
Method	BLASTX
NCBI GI	g2924515
BLAST score	243
E value	1.0e-20
Match length	108
% identity	44
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]
Seq. No.	237266
Seq. ID	uC-gsronu33B103e06b1
Method	BLASTX
NCBI GI	g4510347
BLAST score	428
E value	2.0e-42
Match length	117
% identity	69
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237267
Seq. ID	uC-gsronu33B103g01b1
Method	BLASTX
NCBI GI	g3033375
BLAST score	208
E value	1.0e-16
Match length	66
% identity	58
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
Seq. No.	237268
Seq. ID	uC-gsronu33B104a01b1
Method	BLASTX
NCBI GI	g124429
BLAST score	667
E value	3.0e-70

E value 1.0e-51
 Match length 152
 % identity 59
 NCBI Description (AC005917) putative senescence-associated protein 5
 [Arabidopsis thaliana]

Seq. No. 237274
 Seq. ID uC-gsronu33B104c11b1
 Method BLASTX
 NCBI GI g3292817
 BLAST score 433
 E value 7.0e-43
 Match length 128
 % identity 70
 NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237275
 Seq. ID uC-gsronu33B104d10b1
 Method BLASTX
 NCBI GI g2088648
 BLAST score 268
 E value 9.0e-24
 Match length 84
 % identity 65
 NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237276
 Seq. ID uC-gsronu33B104e05b1
 Method BLASTX
 NCBI GI g4262233
 BLAST score 233
 E value 1.0e-19
 Match length 98
 % identity 53
 NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237277
 Seq. ID uC-gsronu33B104e11b1
 Method BLASTX
 NCBI GI g4090259
 BLAST score 213
 E value 3.0e-17
 Match length 56
 % identity 66
 NCBI Description (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga
 menziesii]

Seq. No. 237278
 Seq. ID uC-gsronu33B104f04b1
 Method BLASTX
 NCBI GI g2586082
 BLAST score 238
 E value 1.0e-29
 Match length 156
 % identity 48
 NCBI Description (U72725) retrofit [Oryza longistaminata]

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Seq. No.	237279
Seq. ID	uC-gsronu33B104f05b1
Method	BLASTX
NCBI GI	g3776025
BLAST score	620
E value	9.0e-65
Match length	144
% identity	83
NCBI Description	(AJ010474) RNA helicase [Arabidopsis thaliana]
Seq. No.	237280
Seq. ID	uC-gsronu33B104f09b1
Method	BLASTX
NCBI GI	g1813891
BLAST score	152
E value	4.0e-10
Match length	38
% identity	87
NCBI Description	(Y10749) 1-aminocyclopropane-1-carboxylate oxidase [Betula pendula]
Seq. No.	237281
Seq. ID	uC-gsronu33B104h01b1
Method	BLASTX
NCBI GI	g1706282
BLAST score	355
E value	1.0e-33
Match length	101
% identity	64
NCBI Description	DISEASE RESISTANCE RESPONSE PROTEIN 206 >gi_508844 (U11716) disease resistance response protein 206-d [Pisum sativum]
Seq. No.	237282
Seq. ID	uC-gsronu33B106b08b2
Method	BLASTX
NCBI GI	g2760844
BLAST score	224
E value	3.0e-18
Match length	68
% identity	59
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237283
Seq. ID	uC-gsronu33B106b09b2
Method	BLASTX
NCBI GI	g2244996
BLAST score	572
E value	5.0e-59
Match length	136
% identity	79
NCBI Description	(Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]
Seq. No.	237284
Seq. ID	uC-gsronu33B106b12b2
Method	BLASTX
NCBI GI	g4432836

Seq. ID	uC-gsronu33B107c01b1
Method	BLASTX
NCBI GI	g2952338
BLAST score	284
E value	3.0e-25
Match length	61
% identity	80
NCBI Description	(AF050200) submergence induced protein 2 [Oryza sativa]
Seq. No.	237296
Seq. ID	uC-gsronu33B107e04b1
Method	BLASTX
NCBI GI	g2660670
BLAST score	268
E value	2.0e-23
Match length	118
% identity	38
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
Seq. No.	237297
Seq. ID	uC-gsronu33B107e05b1
Method	BLASTX
NCBI GI	g2499606
BLAST score	556
E value	3.0e-75
Match length	146
% identity	95
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2) (ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2 [Arabidopsis thaliana]
Seq. No.	237298
Seq. ID	uC-gsronu33B107e09b1
Method	BLASTX
NCBI GI	g4235430
BLAST score	154
E value	2.0e-10
Match length	63
% identity	54
NCBI Description	(AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.	237299
Seq. ID	uC-gsronu33B107f03b1
Method	BLASTX
NCBI GI	g2459442
BLAST score	155
E value	3.0e-10
Match length	66
% identity	52
NCBI Description	(AC002332) putative DNA-binding protein PD1 [Arabidopsis thaliana]
Seq. No.	237300
Seq. ID	uC-gsronu33B107f10b1
Method	BLASTX
NCBI GI	g2244822

NCBI Description (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No. 237306
Seq. ID uC-gsronu33B108c03b1
Method BLASTX
NCBI GI g3915023
BLAST score 481
E value 2.0e-48
Match length 145
% identity 67
NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1
(UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1)
>gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate
synthase [Citrus unshiu]

Seq. No. 237307
Seq. ID uC-gsronu33B108c05b1
Method BLASTX
NCBI GI g4467128
BLAST score 572
E value 4.0e-59
Match length 137
% identity 74
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 237308
Seq. ID uC-gsronu33B108c10b1
Method BLASTX
NCBI GI g729723
BLAST score 188
E value 4.0e-14
Match length 118
% identity 33
NCBI Description PEROXISOMAL FARNESYLATED PROTEIN 33 AND HOUSEKEEPING
PROTEIN) >gi_551250_emb_CAA53225_ (X75535) house keeping
gene 33 [Homo sapiens] >gi_2570023_emb_CAA70257_ (Y09048)
PxP protein [Homo sapiens] >gi_4521235_dbj_BAA76291.1_
(AB018541) PEX19 [Homo sapiens]
>gi_4506339_ref_NP_002848.1_pPXP peroxisomal farnesylated
protein

Seq. No. 237309
Seq. ID uC-gsronu33B108e04b1
Method BLASTX
NCBI GI g3461820
BLAST score 481
E value 2.0e-48
Match length 143
% identity 71
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 237310
Seq. ID uC-gsronu33B108e12b1
Method BLASTX
NCBI GI g1263291
BLAST score 477
E value 4.0e-48

Seq. No. 237316
 Seq. ID uC-gsronu33B109d04b1
 Method BLASTX
 NCBI GI g3033375
 BLAST score 343
 E value 3.0e-32
 Match length 139
 % identity 50
 NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No. 237317
 Seq. ID uC-gsronu33B109e08b1
 Method BLASTX
 NCBI GI g4508079
 BLAST score 258
 E value 2.0e-22
 Match length 98
 % identity 50
 NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 237318
 Seq. ID uC-gsronu33B109e09b1
 Method BLASTX
 NCBI GI g1703200
 BLAST score 323
 E value 6.0e-30
 Match length 98
 % identity 66
 NCBI Description PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No. 237319
 Seq. ID uC-gsronu33B109f08b1
 Method BLASTX
 NCBI GI g4218187
 BLAST score 196
 E value 5.0e-15
 Match length 55
 % identity 40
 NCBI Description (AJ010165) leghemoglobin activating factor [Glycine max]

Seq. No. 237320
 Seq. ID uC-gsronu33B109g07b1
 Method BLASTX
 NCBI GI g3157933
 BLAST score 565
 E value 3.0e-58
 Match length 141
 % identity 69
 NCBI Description (AC002131) Contains similarity to box helicases gb_U29097 from C. elegans and to the ENBP1 gene product gb_X95995 from Vicia sativa. [Arabidopsis thaliana]

NCBI GI g3122367
 BLAST score 151
 E value 6.0e-10
 Match length 98
 % identity 36
 NCBI Description LIGATIN >gi_1377880 (U58337) ligatin [Mus musculus]

Seq. No. 237332
 Seq. ID uC-gsronu33B110h10b1
 Method BLASTX
 NCBI GI g951427
 BLAST score 434
 E value 5.0e-43
 Match length 109
 % identity 73
 NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus communis]

Seq. No. 237333
 Seq. ID uC-gsronu33B111a07b1
 Method BLASTX
 NCBI GI g3549666
 BLAST score 144
 E value 4.0e-09
 Match length 40
 % identity 70
 NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 237334
 Seq. ID uC-gsronu33B111b03b1
 Method BLASTX
 NCBI GI g1345644
 BLAST score 439
 E value 1.0e-43
 Match length 116
 % identity 72
 NCBI Description CYTOCHROME P450 86A1 (CYPLXXXVI) >gi_940446_emb_CAA62082_ (X90458) cytochrome p450 [Arabidopsis thaliana]

Seq. No. 237335
 Seq. ID uC-gsronu33B111c04b1
 Method BLASTX
 NCBI GI g2344887
 BLAST score 207
 E value 2.0e-16
 Match length 57
 % identity 70
 NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 237336
 Seq. ID uC-gsronu33B111c09b1
 Method BLASTX
 NCBI GI g4206208
 BLAST score 231
 E value 4.0e-19
 Match length 97
 % identity 46

Seq. No. 237347
 Seq. ID uC-gsronu33B113c08b1
 Method BLASTX
 NCBI GI g1407705
 BLAST score 593
 E value 1.0e-61
 Match length 145
 % identity 75
 NCBI Description (U60202) lipoxygenase [Solanum tuberosum]

Seq. No. 237348
 Seq. ID uC-gsronu33B113c12b1
 Method BLASTX
 NCBI GI g3786012
 BLAST score 366
 E value 5.0e-35
 Match length 130
 % identity 52
 NCBI Description (AC005499) putative acid phosphatase [Arabidopsis thaliana]

Seq. No. 237349
 Seq. ID uC-gsronu33B113d10b1
 Method BLASTX
 NCBI GI g1086147
 BLAST score 331
 E value 6.0e-31
 Match length 80
 % identity 72
 NCBI Description protein S2 - Phalaris coerulescens >gi_556833_emb_CAA57520_ (X81992) S2 [Phalaris coerulescens]

Seq. No. 237350
 Seq. ID uC-gsronu33B113e01b1
 Method BLASTX
 NCBI GI g4539369
 BLAST score 290
 E value 3.0e-26
 Match length 85
 % identity 68
 NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 237351
 Seq. ID uC-gsronu33B113f01b1
 Method BLASTX
 NCBI GI g3757514
 BLAST score 408
 E value 6.0e-40
 Match length 80
 % identity 95
 NCBI Description (AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No. 237352
 Seq. ID uC-gsronu33B113f03b1
 Method BLASTX
 NCBI GI g417073
 BLAST score 518

E value 6.0e-53
 Match length 116
 % identity 84
 NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
 >gi_484529_pir_JQ1977 glutamate synthase (NADH) (EC
 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate
 synthase [Medicago sativa]

Seq. No. 237353
 Seq. ID uC-gsronu33B113f10b1
 Method BLASTX
 NCBI GI g3367593
 BLAST score 198
 E value 3.0e-15
 Match length 56
 % identity 59
 NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
 >gi_3805841_emb_CAA21461_ (AL031986) putative protein
 [Arabidopsis thaliana]

Seq. No. 237354
 Seq. ID uC-gsronu33B113f11b1
 Method BLASTX
 NCBI GI g2500380
 BLAST score 572
 E value 4.0e-59
 Match length 105
 % identity 100
 NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir_JC4923 ribosomal
 protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal
 protein L44 isoform a [Gossypium hirsutum] >gi_1553131
 (U64678) ribosomal protein L44 isoform b [Gossypium
 hirsutum]

Seq. No. 237355
 Seq. ID uC-gsronu33B113g07b1
 Method BLASTX
 NCBI GI g1706282
 BLAST score 434
 E value 6.0e-43
 Match length 127
 % identity 61
 NCBI Description DISEASE RESISTANCE RESPONSE PROTEIN 206 >gi_508844 (U11716)
 disease resistance response protein 206-d [Pisum sativum]

Seq. No. 237356
 Seq. ID uC-gsronu33B113g08b1
 Method BLASTX
 NCBI GI g861170
 BLAST score 699
 E value 5.0e-74
 Match length 145
 % identity 97
 NCBI Description (X03697) heat shock protein 70 [Zea mays]

Seq. No. 237357
 Seq. ID uC-gsronu33B113g11b1

Seq. ID uC-gsronu33B116a05b1
 Method BLASTX
 NCBI GI g1212759
 BLAST score 254
 E value 8.0e-22
 Match length 47
 % identity 89
 NCBI Description (X89192) DNA binding protein [Arabidopsis thaliana]

Seq. No. 237369
 Seq. ID uC-gsronu33B116a06b1
 Method BLASTX
 NCBI GI g4455293
 BLAST score 359
 E value 4.0e-34
 Match length 133
 % identity 60
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 237370
 Seq. ID uC-gsronu33B116b08b1
 Method BLASTX
 NCBI GI g3395441
 BLAST score 247
 E value 4.0e-21
 Match length 65
 % identity 68
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 237371
 Seq. ID uC-gsronu33B116c01b1
 Method BLASTX
 NCBI GI g1001649
 BLAST score 229
 E value 5.0e-19
 Match length 116
 % identity 47
 NCBI Description (D64002) DNA gyrase A subunit [Synechocystis sp.]

Seq. No. 237372
 Seq. ID uC-gsronu33B116c04b1
 Method BLASTX
 NCBI GI g336392
 BLAST score 271
 E value 7.0e-24
 Match length 89
 % identity 66
 NCBI Description (J05215) ribosomal protein S17 [Arabidopsis thaliana]

Seq. No. 237373
 Seq. ID uC-gsronu33B116c05b1
 Method BLASTX
 NCBI GI g4455330
 BLAST score 323
 E value 6.0e-30
 Match length 149
 % identity 46

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thaliana]

Seq. No. 237379
 Seq. ID uC-gsronu33B116g03b1
 Method BLASTX
 NCBI GI g3176072
 BLAST score 133
 E value 4.0e-16
 Match length 52
 % identity 88
 NCBI Description (AJ002485) protein phosphatase 1, catalytic beta subunit [Medicago sativa]

Seq. No. 237380
 Seq. ID uC-gsronu33B116g04b1
 Method BLASTX
 NCBI GI g3786011
 BLAST score 678
 E value 2.0e-71
 Match length 149
 % identity 85
 NCBI Description (AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No. 237381
 Seq. ID uC-gsronu33B116h01b1
 Method BLASTX
 NCBI GI g2809262
 BLAST score 257
 E value 2.0e-22
 Match length 109
 % identity 46
 NCBI Description (AC002560) F21B7.31 [Arabidopsis thaliana]

Seq. No. 237382
 Seq. ID uC-gsronu33B117a07b1
 Method BLASTX
 NCBI GI g3831471
 BLAST score 178
 E value 4.0e-13
 Match length 57
 % identity 56
 NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237383
 Seq. ID uC-gsronu33B117a10b1
 Method BLASTX
 NCBI GI g3818624
 BLAST score 765
 E value 1.0e-81
 Match length 154
 % identity 96
 NCBI Description (AF095912) actin related protein 2; ARP2 [Arabidopsis thaliana]

Seq. No. 237384
 Seq. ID uC-gsronu33B117c04b1

Method BLASTX
 NCBI GI g2262113
 BLAST score 191
 E value 2.0e-14
 Match length 147
 % identity 40
 NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 237385
 Seq. ID uC-gsronu33B117c09b1
 Method BLASTX
 NCBI GI g3924597
 BLAST score 145
 E value 4.0e-09
 Match length 53
 % identity 57
 NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 237386
 Seq. ID uC-gsronu33B117d08b1
 Method BLASTX
 NCBI GI g404688
 BLAST score 188
 E value 2.0e-14
 Match length 74
 % identity 47
 NCBI Description (L19074) cytochrome P450 [Catharanthus roseus]

Seq. No. 237387
 Seq. ID uC-gsronu33B117d11b1
 Method BLASTX
 NCBI GI g4490303
 BLAST score 249
 E value 3.0e-21
 Match length 53
 % identity 87
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 237388
 Seq. ID uC-gsronu33B117e03b1
 Method BLASTX
 NCBI GI g3831441
 BLAST score 155
 E value 3.0e-10
 Match length 49
 % identity 78
 NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237389
 Seq. ID uC-gsronu33B117e04b1
 Method BLASTX
 NCBI GI g1351014
 BLAST score 206
 E value 1.0e-16
 Match length 41
 % identity 93
 NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)

ribosomal protein S8 [Oryza sativa]

Seq. No. 237390
 Seq. ID uC-gsronu33B117h03b1
 Method BLASTX
 NCBI GI g2443836
 BLAST score 206
 E value 2.0e-16
 Match length 57
 % identity 60
 NCBI Description (AF020793) tonoplast intrinsic protein homolog MSMCP1 [Medicago sativa]

Seq. No. 237391
 Seq. ID uC-gsronu33B121h01b1
 Method BLASTX
 NCBI GI g3914449
 BLAST score 336
 E value 7.0e-32
 Match length 72
 % identity 89
 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No. 237392
 Seq. ID uC-gsronu33B124a03b1
 Method BLASTX
 NCBI GI g1279640
 BLAST score 452
 E value 5.0e-45
 Match length 134
 % identity 62
 NCBI Description (X92204) NAM [Petunia x hybrida]

Seq. No. 237393
 Seq. ID uC-gsronu33B124a06b1
 Method BLASTX
 NCBI GI g3935183
 BLAST score 249
 E value 2.0e-21
 Match length 113
 % identity 49
 NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]

Seq. No. 237394
 Seq. ID uC-gsronu33B124b01b1
 Method BLASTX
 NCBI GI g3540181
 BLAST score 230
 E value 5.0e-19
 Match length 123
 % identity 46
 NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 237395
 Seq. ID uC-gsronu33B124b11b1

Method BLASTX
 NCBI GI g3096945
 BLAST score 435
 E value 4.0e-43
 Match length 107
 % identity 80
 NCBI Description (AL023094) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No. 237396
 Seq. ID uC-gsronu33B124c08b1
 Method BLASTX
 NCBI GI g3927830
 BLAST score 336
 E value 2.0e-31
 Match length 128
 % identity 52
 NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237397
 Seq. ID uC-gsronu33B124e06b1
 Method BLASTX
 NCBI GI g1706958
 BLAST score 716
 E value 5.0e-76
 Match length 135
 % identity 99
 NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 237398
 Seq. ID uC-gsronu33B124e09b1
 Method BLASTX
 NCBI GI g4510345
 BLAST score 282
 E value 4.0e-25
 Match length 63
 % identity 78
 NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 237399
 Seq. ID uC-gsronu33B124e10b1
 Method BLASTX
 NCBI GI g4107276
 BLAST score 151
 E value 8.0e-10
 Match length 36
 % identity 89
 NCBI Description (X98506) acetyl-CoA synthetase [Solanum tuberosum]

Seq. No. 237400
 Seq. ID uC-gsronu33B124f08b1
 Method BLASTX
 NCBI GI g122781
 BLAST score 352
 E value 3.0e-33
 Match length 66
 % identity 97

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 237416

Seq. ID uC-gsronu33B126b01b1

Method BLASTX

NCBI GI g1174592

BLAST score 535

E value 5.0e-55

Match length 103

% identity 97

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin
- garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
sativum]

Seq. No. 237417

Seq. ID uC-gsronu33B126b11b1

Method BLASTX

NCBI GI g4455338

BLAST score 538

E value 3.0e-55

Match length 114

% identity 91

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 237418

Seq. ID uC-gsronu33B126c09b1

Method BLASTX

NCBI GI g3269287

BLAST score 344

E value 1.0e-32

Match length 85

% identity 79

NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 237419

Seq. ID uC-gsronu33B126d08b1

Method BLASTX

NCBI GI g3249068

BLAST score 263

E value 9.0e-23

Match length 128

% identity 42

NCBI Description (AC004473) Contains similarity to zinc-binding protein
(PWA33) gb_L04190 from Pleurodeles waltlii. [Arabidopsis
thaliana]

Seq. No. 237420

Seq. ID uC-gsronu33B126d09b1

Method BLASTX

NCBI GI g1420887

BLAST score 189

E value 3.0e-14

Match length 69

% identity 48

NCBI Description (U34334) non-specific lipid transfer-like protein
[Phaseolus vulgaris]

09684016.101000

Seq. No. 237421
Seq. ID uC-gsronu33B126e02b1
Method BLASTX
NCBI GI g4510346
BLAST score 147
E value 6.0e-10
Match length 40
% identity 68
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237422
Seq. ID uC-gsronu33B126e06b1
Method BLASTX
NCBI GI g1173223
BLAST score 171
E value 2.0e-12
Match length 36
% identity 94
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_454848 (L28831) ribosomal protein S11 [Glycine max]

Seq. No. 237423
Seq. ID uC-gsronu33B126f04b1
Method BLASTX
NCBI GI g4378848
BLAST score 415
E value 1.0e-40
Match length 139
% identity 56
NCBI Description (AF124349) hydrolase [Zymomonas mobilis]

Seq. No. 237424
Seq. ID uC-gsronu33B126f10b1
Method BLASTX
NCBI GI g3478637
BLAST score 282
E value 3.0e-25
Match length 123
% identity 41
NCBI Description (AC005546) R29425_1 [Homo sapiens]

Seq. No. 237425
Seq. ID uC-gsronu33B126g06b1
Method BLASTX
NCBI GI g3885334
BLAST score 209
E value 6.0e-28
Match length 121
% identity 65
NCBI Description (AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No. 237426
Seq. ID uC-gsronu33B126h09b1
Method BLASTX
NCBI GI g283503
BLAST score 138

E value 8.0e-09
 Match length 43
 % identity 70
 NCBI Description tubulin alpha chain - Euplotes vannus (SGC9)
 >gi_9327_emb_CAA77816_ (Z11769) alpha-Tubulin [Euplotes
 vannus]

Seq. No. 237427
 Seq. ID uC-gsronu33B127a01b1
 Method BLASTX
 NCBI GI g2252866
 BLAST score 308
 E value 3.0e-28
 Match length 88
 % identity 80
 NCBI Description (AF013294) contains region of similarity to SYT
 [Arabidopsis thaliana]

Seq. No. 237428
 Seq. ID uC-gsronu33B127a03b1
 Method BLASTX
 NCBI GI g4455207
 BLAST score 270
 E value 3.0e-30
 Match length 88
 % identity 82
 NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 237429
 Seq. ID uC-gsronu33B127a06b1
 Method BLASTX
 NCBI GI g2443887
 BLAST score 222
 E value 2.0e-18
 Match length 61
 % identity 74
 NCBI Description (AC002294) Similar to transcription factor
 gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No. 237430
 Seq. ID uC-gsronu33B127a07b1
 Method BLASTX
 NCBI GI g130771
 BLAST score 173
 E value 2.0e-12
 Match length 82
 % identity 41
 NCBI Description PHOSPHATIDYLINOSITOL TRANSFER PROTEIN ALPHA ISOFORM (PTDINS
 TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-ALPHA)
 >gi_92602_pir_A34391 phosphatidylinositol transfer protein
 - rat >gi_206495 (M25758) phosphatidylinositol transfer
 protein [Rattus norvegicus]

Seq. No. 237431
 Seq. ID uC-gsronu33B127a08b1
 Method BLASTX
 NCBI GI g2662343

Method BLASTX
NCBI GI g4467158
BLAST score 293
E value 2.0e-26
Match length 148
% identity 50
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 237442
Seq. ID uC-gsronu33B129g05b1
Method BLASTX
NCBI GI g1805254
BLAST score 409
E value 5.0e-40
Match length 89
% identity 83
NCBI Description (U62622) monogalactosyldiacylglycerol synthase [Cucumis sativus]

Seq. No. 237443
Seq. ID uC-gsronu33B129g09b1
Method BLASTX
NCBI GI g1352442
BLAST score 307
E value 6.0e-28
Match length 75
% identity 75
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_1002917 (U34598) p28 [Oryza sativa]

Seq. No. 237444
Seq. ID uC-gsronu33B129h05b1
Method BLASTX
NCBI GI g4545262
BLAST score 215
E value 3.0e-17
Match length 48
% identity 85
NCBI Description (AF118230) metallothionein-like protein [Gossypium hirsutum]

Seq. No. 237445
Seq. ID uC-gsronu33B129h06b1
Method BLASTX
NCBI GI g4454484
BLAST score 383
E value 8.0e-37
Match length 120
% identity 62
NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No. 237446
Seq. ID uC-gsronu33B130e03b1
Method BLASTX

NCBI GI	g629483
BLAST score	279
E value	9.0e-25
Match length	106
% identity	55
NCBI Description	gene 1-Sc3 protein - European white birch >gi_534898_emb_CAA54696 (X77601) 1 Sc-3 [Betula pendula] >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula pendula]
Seq. No.	237447
Seq. ID	uC-gsronu33B130e05b1
Method	BLASTX
NCBI GI	g3157949
BLAST score	170
E value	6.0e-12
Match length	41
% identity	63
NCBI Description	(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb_Z28697 from Nicotiana tabacum. ESTs gb_Z18185 and gb_AA605362 come from this gene. [Arabidopsis thaliana]
Seq. No.	237448
Seq. ID	uC-gsronu33B130e06b1
Method	BLASTX
NCBI GI	g4510383
BLAST score	347
E value	1.0e-32
Match length	111
% identity	65
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.	237449
Seq. ID	uC-gsronu33B130e08b1
Method	BLASTX
NCBI GI	g4138583
BLAST score	330
E value	3.0e-31
Match length	73
% identity	88
NCBI Description	(Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
Seq. No.	237450
Seq. ID	uC-gsronu33B130e10b1
Method	BLASTX
NCBI GI	g1652327
BLAST score	267
E value	3.0e-23
Match length	134
% identity	46
NCBI Description	(D90904) hypothetical protein [Synechocystis sp.]
Seq. No.	237451
Seq. ID	uC-gsronu33B130f01b1
Method	BLASTX
NCBI GI	g1345793
BLAST score	318

E value 6.0e-30
 Match length 63
 % identity 97
 NCBI Description CHALCONE SYNTHASE 3 (NARINGENIN-CHALCONE SYNTHASE 3)
 >gi_1084446_pir_S55464 chalcone synthase 3 - gerbera
 hybrid >gi_1362143_pir_S56701 chalcone synthase 3 -
 gerbera hybrid >gi_853932_emb_CAA86220_ (Z38098) chalcone
 synthase [Gerbera hybrida]

Seq. No. 237452
 Seq. ID uC-gsronu33B130f10b1
 Method BLASTX
 NCBI GI g4249388
 BLAST score 326
 E value 2.0e-30
 Match length 87
 % identity 71
 NCBI Description (AC005966) Similar to gb_AF025438 Opa-interacting protein
 (OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 237453
 Seq. ID uC-gsronu33B130h04b1
 Method BLASTX
 NCBI GI g2191175
 BLAST score 266
 E value 2.0e-23
 Match length 113
 % identity 50
 NCBI Description (AF007270) A_IG002P16.24 gene product [Arabidopsis
 thaliana]

Seq. No. 237454
 Seq. ID uC-gsronu33B130h10b1
 Method BLASTX
 NCBI GI g3738297
 BLAST score 156
 E value 6.0e-11
 Match length 43
 % identity 13
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 237455
 Seq. ID uC-gsronu33B132a08b1
 Method BLASTX
 NCBI GI g3661610
 BLAST score 138
 E value 7.0e-09
 Match length 60
 % identity 43
 NCBI Description (AF092565) splicing factor Prp8 [Homo sapiens]

Seq. No. 237456
 Seq. ID uC-gsronu33B132b09b1
 Method BLASTX
 NCBI GI g100226
 BLAST score 182
 E value 3.0e-16

Match length 142
 % identity 39
 NCBI Description hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf_1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No. 237457
 Seq. ID uC-gsronu33B132b10b1
 Method BLASTX
 NCBI GI g4455159
 BLAST score 337
 E value 7.0e-32
 Match length 95
 % identity 64
 NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 237458
 Seq. ID uC-gsronu33B132e02b1
 Method BLASTX
 NCBI GI g3128203
 BLAST score 488
 E value 3.0e-49
 Match length 138
 % identity 68
 NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 237459
 Seq. ID uC-gsronu33B132f06b1
 Method BLASTX
 NCBI GI g1351279
 BLAST score 497
 E value 2.0e-50
 Match length 116
 % identity 84
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_602590_emb_CAA58230_ (X83227) triosephosphate isomerase [Petunia x hybrida]

Seq. No. 237460
 Seq. ID uC-gsronu33B132f12b1
 Method BLASTX
 NCBI GI g3738285
 BLAST score 301
 E value 2.0e-27
 Match length 64
 % identity 83
 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 237461
 Seq. ID uC-gsronu33B132g02b1
 Method BLASTX
 NCBI GI g4567226
 BLAST score 183
 E value 2.0e-13
 Match length 73
 % identity 55

Method BLASTX
 NCBI GI g1777443
 BLAST score 407
 E value 8.0e-40
 Match length 91
 % identity 85
 NCBI Description (U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310)
 DNA-binding protein CCA1 [Arabidopsis thaliana] >gi_4090569
 (U79156) CCA1 [Arabidopsis thaliana]

Seq. No. 237468
 Seq. ID uC-gsronu33B134c03b1
 Method BLASTX
 NCBI GI g3461835
 BLAST score 502
 E value 5.0e-51
 Match length 123
 % identity 79
 NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]
 >gi_3927840 (AC005727) putative protein kinase [Arabidopsis
 thaliana]

Seq. No. 237469
 Seq. ID uC-gsronu33B134d09b1
 Method BLASTX
 NCBI GI g266989
 BLAST score 289
 E value 5.0e-26
 Match length 93
 % identity 62
 NCBI Description GTP-BINDING PROTEIN SAR1B >gi_322517_pir_S28603
 GTP-binding protein - Arabidopsis thaliana >gi_166734
 (M95795) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 237470
 Seq. ID uC-gsronu33B134e05b1
 Method BLASTX
 NCBI GI g3395756
 BLAST score 168
 E value 3.0e-18
 Match length 91
 % identity 56
 NCBI Description (U76297) plantacyanin [Arabidopsis thaliana] >gi_3461812
 (AC004138) putative basic blue protein [Arabidopsis
 thaliana]

Seq. No. 237471
 Seq. ID uC-gsronu33B134e08b1
 Method BLASTX
 NCBI GI g3702343
 BLAST score 271
 E value 5.0e-24
 Match length 114
 % identity 53
 NCBI Description (AC005397) putative homeotic gene regulator [Arabidopsis
 thaliana]

Method BLASTX
 NCBI GI g2281090
 BLAST score 458
 E value 7.0e-46
 Match length 132
 % identity 70
 NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237478
 Seq. ID uC-gsronu33B136d06b1
 Method BLASTX
 NCBI GI g4006896
 BLAST score 280
 E value 4.0e-25
 Match length 113
 % identity 60
 NCBI Description (Z99708) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 237479
 Seq. ID uC-gsronu33B136e12b1
 Method BLASTX
 NCBI GI g2760839
 BLAST score 333
 E value 4.0e-31
 Match length 134
 % identity 51
 NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 237480
 Seq. ID uC-gsronu33B136f02b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 7.0e-15
 Match length 47
 % identity 68
 NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No. 237481
 Seq. ID uC-gsronu33B136f04b1
 Method BLASTX
 NCBI GI g2911799
 BLAST score 494
 E value 6.0e-50
 Match length 121
 % identity 83
 NCBI Description (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No. 237482
 Seq. ID uC-gsronu33B136f09b1
 Method BLASTX
 NCBI GI g4185819
 BLAST score 192
 E value 2.0e-14
 Match length 47

NCBI Description (X95269) LRR protein [*Lycopersicon esculentum*]

Seq. No. 237488
Seq. ID uC-gsronu33B137a06b1
Method BLASTX
NCBI GI g2781345
BLAST score 507
E value 2.0e-51
Match length 149
% identity 62

NCBI Description (AC003113) F24O1.2 [*Arabidopsis thaliana*]

Seq. No. 237489
Seq. ID uC-gsronu33B137b02b1
Method BLASTX
NCBI GI g2995405
BLAST score 268
E value 2.0e-23
Match length 75
% identity 65

NCBI Description (Y12432) polyprotein [*Ananas comosus*]

Seq. No. 237490
Seq. ID uC-gsronu33B137b08b1
Method BLASTX
NCBI GI g3183640
BLAST score 191
E value 9.0e-15
Match length 35
% identity 97

NCBI Description (AJ005869) transmembrane channel protein [*Cicer arietinum*]

Seq. No. 237491
Seq. ID uC-gsronu33B137c06b1
Method BLASTX
NCBI GI g3292823
BLAST score 175
E value 1.0e-12
Match length 105
% identity 36

NCBI Description (AL031018) putative protein [*Arabidopsis thaliana*]

Seq. No. 237492
Seq. ID uC-gsronu33B137c07b1
Method BLASTX
NCBI GI g1840045
BLAST score 148
E value 2.0e-09
Match length 153
% identity 28

NCBI Description (U49082) transporter protein [*Homo sapiens*]

Seq. No. 237493
Seq. ID uC-gsronu33B137c08b1
Method BLASTX
NCBI GI g4538920
BLAST score 275

BLAST score 345
 E value 2.0e-32
 Match length 154
 % identity 49
 NCBI Description (X86021) potassium channel [Solanum tuberosum]

Seq. No. 237504
 Seq. ID uC-gsronu33B138b02b1
 Method BLASTX
 NCBI GI g3193316
 BLAST score 569
 E value 8.0e-59
 Match length 140
 % identity 80
 NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 237505
 Seq. ID uC-gsronu33B138b06b1
 Method BLASTX
 NCBI GI g2462753
 BLAST score 391
 E value 3.0e-38
 Match length 82
 % identity 83
 NCBI Description (AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 237506
 Seq. ID uC-gsronu33B138b11b1
 Method BLASTX
 NCBI GI g2088648
 BLAST score 191
 E value 8.0e-15
 Match length 80
 % identity 50
 NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237507
 Seq. ID uC-gsronu33B138e05b1
 Method BLASTX
 NCBI GI g2982331
 BLAST score 316
 E value 3.0e-29
 Match length 64
 % identity 98
 NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]

Seq. No. 237508
 Seq. ID uC-gsronu33B138f04b1
 Method BLASTX
 NCBI GI g2827002
 BLAST score 255
 E value 3.0e-22
 Match length 51
 % identity 100
 NCBI Description (AF005993) HSP70 [Triticum aestivum]

Seq. No.	237519
Seq. ID	uC-gsronu33B139c10b1
Method	BLASTX
NCBI GI	g3121739
BLAST score	311
E value	2.0e-28
Match length	144
% identity	16
NCBI Description	ANGIO-ASSOCIATED MIGRATORY CELL PROTEIN >gi_2134759_pir_I39383 angio-associated migratory cell protein - human >gi_870803 (M95627) angio-associated migratory cell protein [Homo sapiens] >gi_4557229_ref_NP_001078.1_pAAMP_ angio-associated, migratory cell protein
Seq. No.	237520
Seq. ID	uC-gsronu33B139c11b1
Method	BLASTX
NCBI GI	g2702272
BLAST score	197
E value	3.0e-15
Match length	69
% identity	17
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana]
Seq. No.	237521
Seq. ID	uC-gsronu33B139d06b1
Method	BLASTX
NCBI GI	g3738327
BLAST score	292
E value	2.0e-26
Match length	97
% identity	65
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]
Seq. No.	237522
Seq. ID	uC-gsronu33B139e08b1
Method	BLASTX
NCBI GI	g3201680
BLAST score	499
E value	1.0e-50
Match length	140
% identity	67
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]
Seq. No.	237523
Seq. ID	uC-gsronu33B139f12b1
Method	BLASTX
NCBI GI	g4538929
BLAST score	394
E value	3.0e-38
Match length	155
% identity	59
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No. 237524
 Seq. ID uC-gsronu33B139g10b1
 Method BLASTX
 NCBI GI g585338
 BLAST score 224
 E value 2.0e-18
 Match length 54
 % identity 81
 NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
 >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza
 sativa]

Seq. No. 237525
 Seq. ID uC-gsronu33B141a06b1
 Method BLASTX
 NCBI GI g3023816
 BLAST score 284
 E value 2.0e-25
 Match length 56
 % identity 96
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_968996 (U31676) glyceraldehyde-3-phosphate
 dehydrogenase [Oryza sativa]

Seq. No. 237526
 Seq. ID uC-gsronu33B141b06b1
 Method BLASTX
 NCBI GI g4056506
 BLAST score 219
 E value 1.0e-17
 Match length 135
 % identity 34
 NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 237527
 Seq. ID uC-gsronu33B141b09b1
 Method BLASTX
 NCBI GI g2832642
 BLAST score 171
 E value 4.0e-12
 Match length 137
 % identity 19
 NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 237528
 Seq. ID uC-gsronu33B141d12b1
 Method BLASTX
 NCBI GI g1706958
 BLAST score 733
 E value 6.0e-78
 Match length 154
 % identity 90
 NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 237529
 Seq. ID uC-gsronu33B141e05b1

Method BLASTX
 NCBI GI g81857
 BLAST score 340
 E value 7.0e-32
 Match length 71
 % identity 90
 NCBI Description IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally controlled tumor protein [Medicago sativa]

Seq. No. 237535
 Seq. ID uC-gsronu33B143a12b1
 Method BLASTX
 NCBI GI g4454043
 BLAST score 499
 E value 1.0e-50
 Match length 151
 % identity 64
 NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 237536
 Seq. ID uC-gsronu33B143c03b1
 Method BLASTX
 NCBI GI g3426039
 BLAST score 447
 E value 1.0e-44
 Match length 126
 % identity 66
 NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 237537
 Seq. ID uC-gsronu33B143c06b1
 Method BLASTX
 NCBI GI g3643607
 BLAST score 326
 E value 1.0e-30
 Match length 83
 % identity 40
 NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 237538
 Seq. ID uC-gsronu33B143c07b1
 Method BLASTX
 NCBI GI g2191165
 BLAST score 209
 E value 1.0e-16
 Match length 82
 % identity 50
 NCBI Description (AF007270) A_IG002P16.14 gene product [Arabidopsis thaliana]

Seq. No. 237539
 Seq. ID uC-gsronu33B143d02b1
 Method BLASTX
 NCBI GI g3548801
 BLAST score 188
 E value 2.0e-14

Match length 129
 % identity 50
 NCBI Description (U54558) translation initiation factor eIF3 p66 subunit
 [Homo sapiens] >gi_4200328_emb_CAA18440_ (AL022313)
 EIF3-P66 [Homo sapiens]
 >gi_4503523_ref_NP_003744.1_pEIF3S7_ UNKNOWN

Seq. No. 237550
 Seq. ID uC-gsronu33B144f09b1
 Method BLASTX
 NCBI GI g2980777
 BLAST score 217
 E value 1.0e-17
 Match length 110
 % identity 41
 NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 237551
 Seq. ID uC-gsronu33B144h03b1
 Method BLASTX
 NCBI GI g2970051
 BLAST score 243
 E value 1.0e-20
 Match length 75
 % identity 63
 NCBI Description (AB012110) ARG10 [Vigna radiata]

Seq. No. 237552
 Seq. ID uC-gsronu33B145c08b1
 Method BLASTX
 NCBI GI g3687223
 BLAST score 160
 E value 8.0e-11
 Match length 38
 % identity 82
 NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237553
 Seq. ID uC-gsronu33B145d10b1
 Method BLASTX
 NCBI GI g548770
 BLAST score 213
 E value 1.0e-28
 Match length 81
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal
 protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
 ribosomal protein L3 [Oryza sativa]

Seq. No. 237554
 Seq. ID uC-gsronu33B145f08b1
 Method BLASTX
 NCBI GI g3046693
 BLAST score 308
 E value 3.0e-28
 Match length 91
 % identity 60

Seq. No.	237560
Seq. ID	uC-gsronu33B146d04b1
Method	BLASTX
NCBI GI	g2894612
BLAST score	372
E value	1.0e-35
Match length	106
% identity	64
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	237561
Seq. ID	uC-gsronu33B146d12b1
Method	BLASTX
NCBI GI	g3935150
BLAST score	337
E value	1.0e-31
Match length	117
% identity	40
NCBI Description	(AC005106) T25N20.14 [Arabidopsis thaliana]
Seq. No.	237562
Seq. ID	uC-gsronu33B146e04b1
Method	BLASTX
NCBI GI	g4580461
BLAST score	354
E value	1.0e-33
Match length	81
% identity	83
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]
Seq. No.	237563
Seq. ID	uC-gsronu33B146e06b1
Method	BLASTX
NCBI GI	g1871192
BLAST score	183
E value	1.0e-13
Match length	114
% identity	45
NCBI Description	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]
Seq. No.	237564
Seq. ID	uC-gsronu33B146f11b1
Method	BLASTX
NCBI GI	g113624
BLAST score	515
E value	2.0e-52
Match length	115
% identity	87
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_22620_emb_CAA46649_(X65742) fructose-bisphosphate aldolase [Spinacia oleracea]
Seq. No.	237565
Seq. ID	uC-gsronu33B146g03b1
Method	BLASTX

from this gene. [Arabidopsis thaliana]

Seq. No. 237581
Seq. ID uC-gsronu33B149a05b1
Method BLASTX
NCBI GI g4185819
BLAST score 192
E value 1.0e-14
Match length 47
% identity 68
NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea batatas]

Seq. No. 237582
Seq. ID uC-gsronu33B149a06b1
Method BLASTX
NCBI GI g3927835
BLAST score 559
E value 1.0e-57
Match length 132
% identity 80
NCBI Description (AC005727) similar to Streptomyces PapA [Arabidopsis thaliana]

Seq. No. 237583
Seq. ID uC-gsronu33B149c12b1
Method BLASTX
NCBI GI g218157
BLAST score 191
E value 1.0e-14
Match length 43
% identity 86
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 237584
Seq. ID uC-gsronu33B149e05b1
Method BLASTX
NCBI GI g1703446
BLAST score 449
E value 9.0e-45
Match length 122
% identity 70
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
>gi_1076292_pir_S53127 asparaginase - Arabidopsis thaliana
>gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No. 237585
Seq. ID uC-gsronu33B149f10b1
Method BLASTX
NCBI GI g2541876
BLAST score 279
E value 1.0e-24
Match length 150
% identity 39
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	237586
Seq. ID	uC-gsronu33B149g08b1
Method	BLASTX
NCBI GI	g4056496
BLAST score	516
E value	1.0e-52
Match length	119
% identity	75
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.	237587
Seq. ID	uC-gsronu33B149g11b1
Method	BLASTX
NCBI GI	g2827141
BLAST score	340
E value	3.0e-32
Match length	65
% identity	91
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	237588
Seq. ID	uC-gsronu33B149h01b1
Method	BLASTX
NCBI GI	g4512705
BLAST score	476
E value	4.0e-48
Match length	105
% identity	89
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	237589
Seq. ID	uC-gsronu33B149h07b1
Method	BLASTX
NCBI GI	g4432855
BLAST score	234
E value	1.0e-19
Match length	116
% identity	53
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]
Seq. No.	237590
Seq. ID	uC-gsronu33B150a11b1
Method	BLASTX
NCBI GI	g2129770
BLAST score	183
E value	1.0e-13
Match length	48
% identity	65
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 237591
 Seq. ID uC-gsronu33B150d06b1
 Method BLASTX
 NCBI GI g1174867
 BLAST score 153
 E value 3.0e-10
 Match length 35
 % identity 83
 NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
 PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
 KD PROTEIN) >gi_633687_emb_CAA55862_(X79275)
 ubiquinol--cytochrome c reductase [Solanum tuberosum]
 >gi_1094912_prf_2107179A cytochrome c
 oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No. 237592
 Seq. ID uC-gsronu33B150d10b1
 Method BLASTX
 NCBI GI g3335366
 BLAST score 218
 E value 2.0e-17
 Match length 76
 % identity 54
 NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 237593
 Seq. ID uC-gsronu33B150d12b1
 Method BLASTX
 NCBI GI g3643082
 BLAST score 149
 E value 1.0e-09
 Match length 67
 % identity 51
 NCBI Description (AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum
 crystallinum]

Seq. No. 237594
 Seq. ID uC-gsronu33B150e01b1
 Method BLASTX
 NCBI GI g3582434
 BLAST score 255
 E value 4.0e-22
 Match length 97
 % identity 58
 NCBI Description (AB017273) low-molecular-weight heat shock protein [Cuscuta
 japonica]

Seq. No. 237595
 Seq. ID uC-gsronu33B150g10b1
 Method BLASTX
 NCBI GI g4455293
 BLAST score 253
 E value 1.0e-21
 Match length 58
 % identity 86
 NCBI Description (AL035528) putative protein [Arabidopsis thaliana]